



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 107534

TO: Phillip Gambel
Location: CM1/9E12
Art Unit: 1644
Thursday, November 06, 2003

Case Serial Number: 09761569

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gambel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

107534

From: STIC-ILL
Sent: Tuesday, November 04, 2003 1:06 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/761569 davis amd

Request for you.

-----Original Message-----

From: Gambel, Phillip
Sent: Tuesday, November 04, 2003 1:01 PM
T : STIC-ILL
Subject: 09/761569 davis amd

stic

please provide a sequence and a sequence interference search for

in paper for

ussn 09/761,569 (Davis et al. amd cytokine / stress mmk)

SEQ ID NO: 2

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 11/5/03
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 108
WWW/Internet: _____
Other (specify): _____

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PR 19-MAY-1995; 95US-0446083.
 PR 19-SEP-1995; 95US-0530950.
 XX (UYMA-) UNIV MASSACHUSETTS.
 PA
 XX Davis RJ, Raingeaud J, Derijard B,
 PI
 XX WPI; 2002-682026/73.
 DR N-PSDB; ABSS3208.
 XX
 PT New human mitogen-activated protein kinase kinase, MKK polypeptide for
 PT identifying reagents that modulate MKK signal transduction pathways, is
 PT capable of phosphorylating human mitogen-activated protein kinase p38
 PT
 XX
 PS Claim 2; Page 15-16; 60pp; English.
 XX
 CC The invention discloses substantially pure human mitogen-activated
 CC protein kinase kinase (MKK) polypeptides having serine, threonine and
 CC tyrosine kinase activity and phosphorylating human mitogen-activated
 CC protein (MAP) kinase p38. A MKK specific antibody is useful for measuring
 CC the synthesis of MKK in a biological test sample, which in turn is useful
 CC for identifying a reagent which modulates MKK synthesis. Methods to
 CC measure the activity and expression of MKK are useful for identifying
 CC reagents which modulate, and preferably inhibit, MKK activity. A method
 CC of treating an MKK-mediated disorder in a patient, by administering a
 CC reagent that modulates MKK activity is useful against disorders such as
 CC ischemic heart disease, kidney failure, oxidative liver damage,
 CC respiratory distress syndrome, heat and radiation burns, septic shock,
 CC rheumatoid arthritis, autoimmune disorders and inflammatory diseases. MKK
 CC polypeptides are useful to produce antibodies that are immunoreactive or
 CC bind epitopes of MKK polypeptides and to screen for reagents that
 CC modulate MKK activity. Reagents that inhibit MKK signal transduction are
 CC useful as therapeutic agents for the treatment of MKK-mediated disorders
 CC and in drug design for elucidation of the specific molecular features
 CC needed to inhibit MKK signal transduction pathways. The sequence
 CC presented is the human MKK3 protein, variation #1.
 CC
 XX
 XX Sequence 318 AA;
 SO
 Query Match 100.0%; Score 1660; DB 23; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1.6e-156;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSKRPAPNPTPPRNLDSTRFTITGDRMFVEADDLVTISLGGAGVGVKRRHQAQSGT 60
 DB 1 MSKRPAPNPTPPRNLDSTRFTITGDRMFVEADDLVTISLGGAGVGVKRRHQAQSGT 60
 QY 61 MAVKRIIRATVNSOQKRLMDLDINMRTVDCFTVTFYFALFREGDVMICMELMDTSLDK 120
 DB 61 MAVKRIIRATVNSOQKRLMDLDINMRTVDCFTVTFYFALFREGDVMICMELMDTSLDK 120
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIYRALHLSKLSVIRHDKVPSNVLINKEGHVMKCP 180
 DB 121 FYRKVLDKNMTIPEDILGEIAVSIYRALHLSKLSVIRHDKVPSNVLINKEGHVMKCP 180
 QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINBELNOKGVNKSVDWSLGTITMELILRPYE 240
 DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINBELNOKGVNKSVDWSLGTITMELILRPYE 240
 QY 241 SWGTFPOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLEMEHPFTLHK 300
 DB 241 SWGTFPOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLEMEHPFTLHK 300
 QY 301 TKKTIDIAAFVKILGEDS 318
 DB 301 TKKTIDIAAFVKILGEDS 318
 RESULT 2
 AAM06318
 ID AAM06318 standard; Protein; 318 AA.
 XX

AC AAM06318;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 XX Human mitogen-activated protein kinase kinase 3.
 DE
 XX Mitogen-activated protein kinase kinase 3; MKK3; MAP;
 KM tyrosine kinase; signal transduction; cytokine; oncoprotein;
 KW stress; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO963642-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 26-JAN-1996; 96WO-US01078.
 XX
 PR 19-SEP-1995; 95US-0530950.
 PR 19-MAY-1995; 95US-0446083.
 XX
 PA (DAVI/) DAVIS R J.
 PA (DERI/) DERIJARD B.
 PA (GUPT/) GUPTA S.
 PA (RAIN/) RAINGEAUD J.
 XX
 PI Davis RJ, Derijard B, Gupta S, Raingeaud J;
 DR WPI; 1997-012035/01.
 DR N-PSDB; AAT43203.
 XX
 PT New mitogen activated protein kinase kinase - useful for treating
 PT ischemic heart disease, kidney failure etc., also for identifying
 PT modulators for treatment of similar conditions
 XX
 XX Claim 2; Fig 4; 104pp; English.
 XX
 CC Novel human mitogen activated protein kinase kinase 3 (MKK3)
 CC (AAM06318) has serine, threonine and tyrosine kinase activity, and
 CC mediates a signal transduction pathway that activates human
 CC mitogen-activated protein (MAP) kinase p38. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT43203) obt'd. from a human
 CC foetal brain library. MKK3 is expressed in all tissues tested, but
 CC partic. in skeletal muscle. Recombinant MKK3 can be produced in
 CC transformed host cells. MKK3 (AAM06318-22) can be used in the
 CC treatment of MKK-related disorders, e.g. ischemic heart disease
 CC and kidney failure, to identify modulators of MKK activity, and
 CC to raise antibodies.
 CC
 XX
 XX Sequence 318 AA;
 SO
 Query Match 99.6%; Score 1653; DB 18; Length 318;
 Best Local Similarity 99.7%; Pred. No. 8.1e-156;
 Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSKRPAPNPTPPRNLDSTRFTITGDRMFVEADDLVTISLGGAGVGVKRRHQAQSGT 60
 DB 1 MSKRPAPNPTPPRNLDSTRFTITGDRMFVEADDLVTISLGGAGVGVKRRHQAQSGT 60
 QY 61 MAVKRIIRATVNSOQKRLMDLDINMRTVDCFTVTFYFALFREGDVMICMELMDTSLDK 120
 DB 61 MAVKRIIRATVNSOQKRLMDLDINMRTVDCFTVTFYFALFREGDVMICMELMDTSLDK 120
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIYRALHLSKLSVIRHDKVPSNVLINKEGHVMKCP 180
 DB 121 FYRKVLDKNMTIPEDILGEIAVSIYRALHLSKLSVIRHDKVPSNVLINKEGHVMKCP 180
 QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINBELNOKGVNKSVDWSLGTITMELILRPYE 240
 DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINBELNOKGVNKSVDWSLGTITMELILRPYE 240
 QY 241 SWGTFPOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLEMEHPFTLHK 300
 DB 241 SWGTFPOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLEMEHPFTLHK 300

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Db      241 SWGTFPOOLKQVVEEPPQLPADRFSPFVDFTAOCLRKPAERMSYLELMEHPFTLHK 300
Qy      301 TKKTDIAAFVKKILGEDS 318
Db      301 TKKTDIAAFVKKILGEDS 318

RESULT 3
AAW97668
ID      AAW97668 standard; Protein; 318 AA.
XX
AC      AAW97668;
XX
DT      10-MAY-1999 (first entry)
XX
DE      Human mitogen activated protein kinase MKK3.
XX
KW      MKK3; mitogen activated protein kinase kinase; MAP kinase kinase;
KW      human; signal transduction; inflammation; psoriasis; AIDS; cancer;
KW      apoptosis; therapy.
XX
OS      Homo sapiens.
XX
PN      W09902547-A1.
XX
PD      21-JAN-1999.
XX
PF      07-JUL-1998; 98WO-US14101.
XX
PR      07-JUL-1997; 97US-0888429.
XX
PA      (UYMA-) UNIV MASSACHUSETTS.
PI      Davis RJ, Tournier C, Whitmarsh A;
XX
DR      WPI; 1999-120771/10.
DR      N-PSDB; AAX07065.
XX
PT      New isolated mitogen-activated protein kinase kinase isoforms - used
PT      to develop products for treating e.g. inflammatory disorders,
PT      oxidative damage, proliferative disorders or autoimmune disorders
XX
XX      Example 1; Page 126-127; 168pp; English.
XX
CC      This polypeptide comprises human mitogen activated protein (MAP)
CC      kinase kinase 3 (MKK3), a 36 kDa protein that phosphorylates p38 but
CC      not JNK1 or ERK2. The amino acid sequence was deduced from an
CC      isolated human brain cDNA clone (see AAX07065). The human MAP kinase
CC      kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),
CC      described in the invention, mediate the transduction of specific
CC      signals from the cell surface to the nucleus along specific
CC      pathways. They are useful for screening reagents which modulate
CC      MKK activity. Such agents can be used to prevent or treat
CC      stress-related disorders, e.g. inflammation, oxidative damage or
CC      stress-related proliferative disorders, e.g. psoriasis, AIDS,
CC      malignancies of e.g. the skin, bone marrow, lung, liver, breast,
CC      gastrointestinal system and genito-urinary tract. Agents which
CC      inhibit the activity or expression of MKK inhibit cell growth or
CC      cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and
CC      polypeptides (see AAW97662-67) are claimed.
XX
SQ      Sequence 318 AA;

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Query Match      99.6%; Score 1653; DB 20; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MSKRPANPTPPRLDSTRFTTIGDRMEVEADLVITISLGRAYGVKVRHAOSGTI 60
Db      1 MSKRPANPTPPRLDSTRFTTIGDRMEVEADLVITISLGRAYGVKVRHAOSGTI 60
Qy      61 MAVERIRATVNSQEQKRLMDLDMRTVDCFYTVTFYGAALFREGDWIMCELMADTSLDK 120
Db      61 MAVERIRATVNSQEQKRLMDLDMRTVDCFYTVTFYGAALFREGDWIMCELMADTSLDK 120

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Db      61 MAVERIRATVNSQEQKRLMDLDMRTVDCFYTVTFYGAALFREGDWIMCELMADTSLDK 120
Qy      121 FYRKVLDRKMTIPEDLIGETAVSVRALHLSLSTVTHDVKRSNTLKNKGHVKKDF 180
Db      121 FYRKVLDRKMTIPEDLIGETAVSVRALHLSLSTVTHDVKRSNTLKNKGHVKKCDF 180
Qy      181 GISGYLVDVSAKTMADACCKPYMAPERINPELNQGVNKSVDVMSLGITMELALRFPYE 240
Db      181 GISGYLVDVSAKTMADACCKPYMAPERINPELNQGVNKSVDVMSLGITMELALRFPYE 240
Qy      241 SWGTFPOOLKQVVEEPPQLPADRFSPFVDFTAOCLRKPAERMSYLELMEHPFTLHK 300
Db      241 SWGTFPOOLKQVVEEPPQLPADRFSPFVDFTAOCLRKPAERMSYLELMEHPFTLHK 300
Qy      301 TKKTDIAAFVKKILGEDS 318
Db      301 TKKTDIAAFVKKILGEDS 318

RESULT 4
AAB31688
ID      AAB31688 standard; Protein; 318 AA.
XX
AC      AAB31688;
XX
DT      30-APR-2001 (first entry)
XX
DE      A human mitogen-activated protein kinase kinase MKK3.
XX
KW      Mitogen-activated protein kinase kinase; MAP kinase kinase; MKK; MKK3;
KW      inflammation; oxidative damage; ischemic heart disease; burn; alcohol;
KW      kidney failure; liver damage; oxidative stress; rheumatoid arthritis;
KW      respiratory distress syndrome; septic shock; autoimmune disorder;
KW      inflammatory disease; proliferative disorder; psoriasis;
KW      acquired immune deficiency syndrome.
XX
OS      Homo sapiens.
XX
PN      US6174676-B1.
XX
PD      16-JAN-2001.
XX
PF      08-SEP-1998; 98US-0149879.
XX
PR      07-APR-1998; 98US-0057009.
PR      19-MAY-1995; 95US-0446083.
PR      19-SEP-1995; 95US-0530950.
XX
PA      (UYMA-) UNIV MASSACHUSETTS.
PI      Davis RJ, Raingeaud J, Dertjard B;
XX
DR      WPI; 2001-181551/18.
DR      N-PSDB; AAF25238.
XX
PT      Identifying mitogen-activating protein kinase activity (MKK), synthesis
PT      or expression modulators, comprises measuring effect of test reagent on
PT      MKK phosphorylation, synthesis or expression after incubation with MKK
XX
XX      Example 1; Fig 4; 59pp; English.
XX
CC      The present sequence represents a human mitogen-activated protein (MAP)
CC      kinase kinase MKK3. The specification describes a method for identifying
CC      a reagent that modulates mitogen-activating MAP kinase kinase (MKK)
CC      activity, synthesis or expression. The method comprises incubating MKK
CC      with the test reagent and measuring the effect of the test reagent on
CC      phosphorylation, MKK synthesis or MKK expression. MKK modulating reagents
CC      identified by the method of the invention are useful for treating or
CC      preventing MKK mediated disorders such as inflammation, oxidative damage,
CC      ischemic heart disease, burns due to heat or radiation, kidney failure,
CC      liver damage due to oxidative stress or alcohol, respiratory distress
CC      syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, and

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other types of inflammatory diseases and stress-related Mxk-mediated CC proliferative disorders such as psoriasis, acquired immune deficiency CC syndrome, malignancies of various tissues of the body, including CC malignancies of the skin, bone marrow, lung, liver, breast etc..

XX Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 22; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60
1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60
DB 1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60

QY 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
DB 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120

QY 121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180
121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180
DB 121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180

QY 181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240
181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240
DB 181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240

QY 241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300
241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300
DB 241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300

QY 301 TKKTDIAAFVKKILGEDS 318
301 TKKTDIAAFVKKILGEDS 318
DB 301 TKKTDIAAFVKKILGEDS 318

RESULT 5
AAG67438
ID AAG67438 standard; Protein: 318 AA.

AC AAG67438;
DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human polypeptide.

XX Human; protein kinase; protein phosphatase; signal transduction;
XX Intracellular signalling pathway.

OS Homo sapiens.

FN W0200109345-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05060.

PR 29-JUL-1999; 99JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX (HELI-) HELIX RES INST.

PI Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Iehi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

PI Seno C, Nezu J;

PI WPI; 2001-564736/63.

PT New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal

PT disorders associated with the expression or function of these enzymes -
XX Example 4; Page 207-210; 336pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases.
CC The polypeptides are expected to participate in signal transduction
CC in cells. The kinase phosphatases are connected with intracellular
CC signalling pathways. Antisense oligonucleotides and compounds
CC identified by screening (agonists or antagonists) can be used to
CC treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development. The present sequence
CC represents a polypeptide, used in the course of the invention.

XX Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 22; Length 318;
Best Local Similarity 99.7%; Pred. No. 8.1e-156;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60
1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60
DB 1 MSKPAPNPPTPRNLDSTRFTITIGDRMFVEADLVITSELGAGVGVKXVHAQSGTI 60

QY 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
DB 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120

QY 121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180
121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180
DB 121 FYRKVLDKMTIPEDILGEIAVSIVRALHLSKLSVIRHDVPSNVLINKEGHVXKCDF 180

QY 181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240
181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240
DB 181 GISGYLVDSYAKTMDAGCKPYMAPERINPELNQGVNKSVDWSLGITMIEMAILRPYE 240

QY 241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300
241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300
DB 241 SWGTFPQOLKQVVEEESPQLPADRFSPFVDFTAQCLRNKPAERMSYLELMEHPFTLHK 300

QY 301 TKKTDIAAFVKKILGEDS 318
301 TKKTDIAAFVKKILGEDS 318
DB 301 TKKTDIAAFVKKILGEDS 318

RESULT 6
AAG67617
ID AAG67617 standard; Protein: 318 AA.

AC AAG67617;

DT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human protein.

XX Human; protein kinase; protein phosphatase; signal transduction.

OS Homo sapiens.

FN W0200109316-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05061.

PR 29-JUL-1999; 99JP-0248036.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

XX (HELI-) HELIX RES INST.

QY 301 TTKTDIAAFVKILGEDS 318
 DB 301 TTKTDIAAFVKILGEDS 318

RESULT 8

AAU80372
 ID AAU80372 standard; Protein; 318 AA.

AAU80372;

30-JUL-2002 (first entry)

Human cellular kinase MKK3 protein.

Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2.

Homo sapiens.

EPI201765-A2.

02-MAY-2002.

15-OCT-2001; 2001EP-0124604.

16-OCT-2000; 2000US-240750P.

(AXXI-) AXXIMA PHARM AG.

Schubert D, Habenberger P, Stein-Gerlach M, Bevec D;

WPI; 2002-373930/41.

N-PSDB; ABR51172.

Identifying agents for treatment or prevention of cytomegalovirus

infection, comprises contacting test compound with cellular kinase and

detecting change in cellular kinase activity -

disclosure; Page 38-39; 49pp; English.

The present invention relates to a new method for identifying compounds

for treating and/or preventing cytomegalovirus (CMV) infection and/or

related diseases. The method of the invention comprises contacting a

test compound with at least one of the cellular kinases RICK, RIP,

Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in

kinase activity. The method of the invention can be used to treat and/or

prevent CMV infections and related diseases. Oligonucleotides that can

detect the specified kinases can also be used for diagnosis of infection.

The present amino acid sequence represents the human cellular kinase MKK3

protein of the invention, as described above.

Sequence 318 AA;

Query Match 99.6%; Score 1653; DB 23; Length 318;

Best Local Similarity 99.7%; Pred. No. 8.1e-156;

Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MSKPPAPNPPTPRNLDSTRTITIGDRMFEVADLVITISLGGAGVVEKVRHAQSGTI 60

1 MSKPPAPNPPTPRNLDSTRTITIGDRMFEVADLVITISLGGAGVVEKVRHAQSGTI 60

1 MSKPPAPNPPTPRNLDSTRTITIGDRMFEVADLVITISLGGAGVVEKVRHAQSGTI 60

DB 181 GISGYLVDSVAKTMADGCKPYMAPERINPELNQGYVAKSDVSLGITMIEMALRPPE 240

QY 241 SMGTFPOOLKQVVEEPPOLPADRSPFVDDTAQTLKGRNPARMSYELMEHPFTLTK 300

DB 241 SMGTFPOOLKQVVEEPPOLPADRSPFVDDTAQTLKGRNPARMSYELMEHPFTLTK 300

QY 301 TTKTDIAAFVKILGEDS 318

DB 301 TTKTDIAAFVKILGEDS 318

RESULT 9

ABG12149

ID ABG12149 standard; Protein; 359 AA.

ABG12149;

18-FEB-2002 (first entry)

Novel human diagnostic protein #12140.

Human; chromosome mapping; gene mapping; gene therapy; forensic;

food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dzmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

N-PSDB; AAS76336.

New isolated polynucleotide and encoded polypeptides, useful in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits and to assess

biodiversity -

Claim 20; SEQ ID No 42508; 103pp; English.

The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes,

polynucleotide chain reaction (PCR) primers, oligomers, and for chromosome

and gene mapping, and in recombinant production of (II). The

polynucleotides are also used in diagnostics as expressed sequence tags

for identifying expressed genes. (I) is useful in gene therapy techniques

to restore normal activity of (II) or to treat disease states involving

(II). (II) is useful for generating antibodies against it, detecting or

quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

diagnostics involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

amino acid sequences. ABG00010-ABG30377 represent novel human

diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed

specification, but was obtained in electronic format directly from WIPO

at http://wipo.int/pub/published_pat_sequences.

Sequence 359 AA;

Query Match 99.6%; Score 1653; DB 22; Length 359;
 Best Local Similarity 99.7%; Pred. No. 9.6e-156;
 Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKRPANPPPPRLDSRTFTITGDRMFVEADLVITISLGRGAYGVKVRRAOSGTI 60
 DB 42 MSKRPANPPPPRLDSRTFTITGDRMFVEADLVITISLGRGAYGVKVRRAOSGTI 101
 QY 61 MAVKRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYFGLFRGQVWICMELMDSLDK 120
 DB 102 MAVKRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYFGLFRGQVWICMELMDSLDK 161
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSYIHRDVPNSVLINKEGHVKKCDF 180
 DB 162 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSYIHRDVPNSVLINKEGHVKKCDF 221
 QY 181 GISGYLVDSVAKTMDACKPYMAPERINPELNQKGVNKSVDWLSGITMELMRLRPEYE 240
 DB 222 GISGYLVDSVAKTMDACKPYMAPERINPELNQKGVNKSVDWLSGITMELMRLRPEYE 281
 QY 241 SMGTFPQOLKQVVEEPPQLPADRFSPFVDFTAOCLRKNPABRMSTLEMEHPFTLHK 300
 DB 282 SMGTFPQOLKQVVEEPPQLPADRFSPFVDFTAOCLRKNPABRMSTLEMEHPFTLHK 341
 QY 301 TKKTIDIAAFVKILGEDS 318
 DB 342 TKKTIDIAAFVKILGEDS 359

RESULT 10
 ID ABG23442 standard; Protein; 359 AA.
 AC ABG23442;
 XX 18-FEB-2002 (first entry)
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #23433.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 XX WPI, 2001-639362/73.
 DR N-PSDB; AAS87629.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensic; gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 53801; 103bp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensic; gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pct_sequences.

XX Sequence 359 AA;
 SQ Sequence 359 AA;

Query Match 93.1%; Score 1546; DB 22; Length 359;
 Best Local Similarity 93.7%; Pred. No. 4.3e-145;
 Matches 298; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSKRPANPPPPRLDSRTFTITGDRMFVEADLVITISLGRGAYGVKVRRAOSGTI 60
 DB 42 MSKRPANPPPPRLDSRTFTITGDRMFVEADLVITISLGRGAYGVKVRRAOSGTI 101
 QY 61 MAVKRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYFGLFRGQVWICMELMDSLDK 120
 DB 102 MAVKRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYFGLFRGQVWICMELMDSLDK 161
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSYIHRDVPNSVLINKEGHVKKCDF 180
 DB 162 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSYIHRDVPNSVLINKEGHVKKCDF 221
 QY 181 GISGYLVDSVAKTMDACKPYMAPERINPELNQKGVNKSVDWLSGITMELMRLRPEYE 240
 DB 222 GISGYLVDSVAKTMDACKPYMAPERINPELNQKGVNKSVDWLSGITMELMRLRPEYE 281
 QY 241 SMGTFPQOLKQVVEEPPQLPADRFSPFVDFTAOCLRKNPABRMSTLEMEHPFTLHK 300
 DB 282 SMGTFPQOLKQVVEEPPQLPADRFSPFVDFTAOCLRKNPABRMSTLEMEHPFTLHK 341
 QY 301 TKKTIDIAAFVKILGEDS 318
 DB 342 TKKTIDIAAFVKILGEDS 359

RESULT 11
 ID ABG79692 standard; Protein; 329 AA.
 AC ABG79692;
 XX 15-NOV-2002 (first entry)
 DT 15-NOV-2002 (first entry)
 DE Tumour involved gene (TIG) splice variant protein, NV-23.
 XX Human; splice variant; tumour-involved gene; TIG;
 KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
 KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
 XX gene therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 PN US2002086384-A1.
 PD 04-JUL-2002.
 XX 13-MAR-2001; 2001US-0805020.
 PF 14-MAR-2000; 2000IL-0135402.
 PR 16-MAY-2000; 2000IL-0136154.

PA (LEVI/) LEVINE Z.
 PA (DAVI/) DAVID A.
 PA (ROMA/) ROMANO C.
 PA (BERN/) BERNSTEIN J.
 XX
 XX
 PI Levine Z, David A, Romano C, Bernstein J;
 DR MPI: 2002-635679/68.
 DR N-PSDB; AB855222.
 XX
 PT Novel nucleic acid sequence, which is an alternative splicing variant
 PT of tumor involved genes, useful for detecting cancer, predisposition to
 PT cancer, for evaluating cancer state and in gene therapy for treating
 PT cancer
 XX
 PS Claim 4; Page 91; 180pp; English.
 XX
 CC The invention discloses isolated human nucleic acid alternative splicing
 CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
 CC polypeptides are useful for determining the level of a nucleic acid or
 CC polypeptide in a biological sample, for detecting a variant nucleic acid
 CC or polypeptide sequence in a biological sample, for determining the level
 CC of variant nucleic acid or polypeptide sequences in a biological sample
 CC and for determining the ratio between the level of variant sequence in a
 CC first biological sample and the level of the original sequence from which
 CC the variant has been varied by alternative splicing in a second
 CC biological sample and for raising antibodies. A pharmaceutical
 CC composition comprising a carrier and the nucleic acid, is useful for
 CC treating diseases (e.g. cancer) that can be ameliorated or cured by
 CC increasing or decreasing the level of the encoded protein. The nucleic
 CC acids are also useful for diagnostic purposes, especially for detecting
 CC cancer or a predisposition to cancer, for evaluating the state or
 CC aggressiveness of cancer disease, in basic research, for understanding
 CC the physiological function of the original TIG, in targeting or
 CC developing pharmaceuticals, for distinguishing various stages in the life
 CC cycle of the same type of cells which may be helpful for the development
 CC of pharmaceuticals for various cancer stages in which cell cycle is
 CC non-normal, for determining mutations in tumour-involved genes and in
 CC gene therapy. The polypeptides are useful for identifying compounds
 CC capable of binding to the variant product and modulating its activity
 CC and for modulating endothelial differentiation and proliferation, as well
 CC as to modulate apoptosis either ex vivo or in vivo. The sequences
 CC presented in AB8796700-AB879705 are the new variants (NV) 1-36 proteins
 CC of the TIGs disclosed.
 CC
 XX
 XX Sequence 329 AA;
 SQ
 Query Match 90.8%; Score 1508; DB 23; Length 329;
 Best Local Similarity 99.3%; Pred. No. 2,3e-141;
 Matches 289; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSKPPAPNPPTPPNLDSTRTITGDRMEFEVADLVITISLGGAGVGVKVRHAOSGTT 60
 DB 30 MSKPPAPNPPTPPNLDSTRTITGDRMEFEVADLVITISLGGAGVGVKVRHAOSGTT 89
 QY 61 MAKRIRATATNSOQKRLMDLDINMRTVDCPTVTFYGLFREGDVMICMELMDTSLDK 120
 DB 90 MAKRIRATATNSOQKRLMDLDINMRTVDCPTVTFYGLFREGDVMICMELMDTSLDK 149
 QY 121 FYRKVLIDKNTIPEDILGEIIVSIVRALBEHLSKLSVIHRDVPKSVNLINKEGHVVKCDF 180
 DB 150 FYRKVLIDKNTIPEDILGEIIVSIVRALBEHLSKLSVIHRDVPKSVNLINKEGHVVKCDF 209
 QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDWSLGTITMELALRRPYE 240
 DB 210 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDWSLGTITMELALRRPYE 269
 QY 241 SMGTPPQOLKOVVEEPPQLPADRFSEFVDFTAQCLRNKPARMSYLEIM 291
 DB 270 SMGTPPQOLKOVVEEPPQLPADRFSEFVDFTAQCLRNKPARMSYLEIM 320

AAW19631
 ID AAW19631 standard; Protein; 334 AA.
 XX
 AC AAW19631;
 XX
 DT 01-SEP-1997 (first entry)
 XX
 DE Human mitogen-activated protein kinase MEK6.
 XX
 KW MEK-6; mitogen-activated protein kinase kinase; MAPKK; p38;
 KW signal transduction; cell proliferation; osteoarthritis; ischaemia;
 KW reperfusion injury; trauma; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; psoriasis;
 KW inflammatory bowel disease; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9722704-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-US20233.
 XX
 PR 20-DEC-1995; 95US-0576240.
 XX
 PA (SIGN-) SIGNAL PHARM INC.
 XX
 PI Stein B, Yang MKH;
 XX
 DR MPI: 1997-341695/31.
 DR N-PSDB; AAT68716.
 XX
 PT Mitogen-activated protein kinase kinase and corresponding DNA -
 PT phosphorylates p38 cascade members; used in the treatment of
 PT immunological-related cell proliferative diseases
 XX
 PS Claim 1; Page 31-33; 67pp; English.
 XX
 CC Human mitogen-activated protein kinase MEK6 (AAW19631) is a
 CC protein capable of modulating the activity of the mitogen-activated
 CC protein kinase p38 (esp. p38-2). Its amino acid sequence was
 CC deduced from a cDNA clone (AAT68716) obtd. from a MOLT-4 cDNA
 CC library. MEK6 is 88% identical to its closest homologue MKK3,
 CC and all relevant kinase subdomains are conserved. MEK6
 CC polypeptides can be produced in transformed or transfected host
 CC cells. MEK6 and its variants, antibodies raised against MEK6, and
 CC MEK6 nucleic acids can be used to modulate (stimulate or inhibit)
 CC phosphorylation of p38 by MEK6 for use in the treatment of diseases
 CC associated with the p38 cascade e.g. immunological-related cell
 CC proliferative diseases and autoimmune diseases, and also to detect
 CC MEK6 kinase activity and identify proteins that interact with MEK6.
 CC
 XX
 XX Sequence 334 AA;
 SQ
 Query Match 81.9%; Score 1359; DB 18; Length 334;
 Best Local Similarity 82.4%; Pred. No. 1.6e-126;
 Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;
 QY 5 PARNPTPPNLDSTRTITGDRMEFEVADLVITISLGGAGVGVKVRHAOSGTTMAVK 64
 DB 23 POTSSTPPRDLDSKACISIGNQNFVEKADLEIMELGGAGVGVKVRHVSQGLMAVK 82
 QY 65 RIRATATNSOQKRLMDLDINMRTVDCPTVTFYGLFREGDVMICMELMDTSLDKFFYRK 124
 DB 83 RIRATATNSOQKRLMDLDINMRTVDCPTVTFYGLFREGDVMICMELMDTSLDKFFYRK 142
 QY 125 VLDKNTIPEDILGEIIVSIVRALBEHLSKLSVIHRDVPKSVNLINKEGHVVKCDFGIGS 184
 DB 143 VIDKQGTIPEDILGKIAVSIIVKALBEHLSKLSVIHRDVPKSVNLINKEGHVVKCDFGIGS 202
 QY 185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDWSLGTITMELALRRPYESWG 244
 DB 203 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDWSLGTITMELALRRPYESWG 262

QY 245 PFQOLKQVVEEPPSPOLPADRFSPFVDFTAQCLRKPAERMSYLELMEHPFTLHKTCT 304
 DB 263 PFQOLKQVVEEPPSPOLPADRFSAFVDFTSQCLKSKSKERPTPELMQHFFTLHESKGT 322
 QY 305 DIAAFVKKIIGE 316
 DB 323 DVASFVKLIIGD 334

RESULT 13
 AAM06319 standard; Protein; 334 AA.
 ID AAM06319
 AC AAM06319;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Human mitogen-activated protein kinase kinase 6.
 XX
 KM Mitogen-activated protein kinase kinase 6; MKK6; MAP;
 KM tyrosine kinase; signal transduction; cytokine; oncoprotein;
 KM stress; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9636642-A1.
 PD 21-NOV-1996.
 PF 26-JAN-1996; 96WO-US01078.
 PR 19-SEP-1995; 95US-0530950.
 PR 19-MAY-1995; 95US-0446083.
 XX
 PA (DAVI/) DAVIS R J.
 PA (DERI/) DERIJARD B.
 PA (GUPT/) GUPTA S.
 PA (RAIN/) RAINGEAUD J.
 XX
 PI Davis RJ, Derijard B, Gupta S, Raingeaud J;
 XX
 DR WPI; 1997-012035/01.
 DR N-PSDB; AAT43204.
 XX
 PT New mitogen activated protein kinase kinase - useful for treating
 PT ischemic heart disease, kidney failure etc., also for identifying
 PT modulators for treatment of similar conditions
 XX
 PS Claim 6; Fig 5; 104pp; English.
 PS
 CC Novel human mitogen activated protein kinase kinase 6 (MKK6)
 CC (AAM06319) has serine, threonine and tyrosine kinase activity, and
 CC mediates a signal transduction pathway that activates human
 CC mitogen-activated protein (MAP) kinase p38. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT43204) obtd. from a human
 CC skeletal muscle library. Recombinant MKK6 can be produced in
 CC transformed host cells. MKK6 (AAM06318-22) are useful in the
 CC treatment of MKK-related disorders, e.g. ischemic heart disease
 CC and kidney failure, for identifying modulators of MKK activity,
 CC and for raising antibodies.
 CC
 XX Sequence 334 AA;
 SO

Query Match 81.9%; Score 1359; DB 18; Length 334;
 Best Local Similarity 82.4%; Pred. No. 1.6e-126;
 Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

QY 5 PAANPPRRRLDSRTFTTIGDRMFVEVADLVITSELGRGAYGVVEKVRAGSGTMAVK 64
 DB 23 PQTSTPPRLDSDACISIGNONFEVADLLEPTIMEIGRAYGVVEKVRHVPSSQIMAVK 82
 QY 65 RIRATVNSQEQKRLMDLDINMRTVDCFYTVTFYGFALFRGQDWICMELMDTSLDKFYRK 124

DB 83 RIRATVNSQEQKRLMDLDINMRTVDCFPFVTFYGFALFRGQDWICMELMDTSLDKFYRK 142
 QY 125 VLDRKNTIPEDDIIIGELAVSVYRALHEHLSKLSYTHRDVKSANVLINKEGVKCCDFEISG 184
 DB 143 VIDRGQTIPEBDIIIGKIAVSVYKALHEHLSKLSYTHRDVKSANVLINLGVKCCDFEISG 202
 QY 185 YLVDVAKTMDAGCKPYMAPERINPELNQGVKSDVWSLGTMTIEMALTRPPYESWG 244
 DB 203 YLVDVAKTMDAGCKPYMAPERINPELNQGVKSDVWSLGTMTIEMALTRPPYESWG 262
 QY 245 PFQOLKQVVEEPPSPOLPADRFSPFVDFTAQCLRKPAERMSYLELMEHPFTLHKTCT 304
 DB 263 PFQOLKQVVEEPPSPOLPADRFSAFVDFTSQCLKSKSKERPTPELMQHFFTLHESKGT 322
 QY 305 DIAAFVKKIIGE 316
 DB 323 DVASFVKLIIGD 334

RESULT 14
 AAM97669 standard; Protein; 334 AA.
 ID AAM97669
 AC AAM97669;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Human mitogen activated protein kinase kinase MKK6.
 XX
 KM MKK6; mitogen activated protein kinase kinase; MAP kinase kinase;
 KM human; signal transduction; inflammation; psoriasis; AIDS; cancer;
 KM apoptosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9902547-A1.
 PD 21-JAN-1999.
 PF 07-JUL-1998; 98WO-US14101.
 PR 07-JUL-1997; 97US-0888429.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Davis RJ, Tournier C, Whitmarsh A;
 XX
 DR WPI; 1999-120771/10.
 DR N-PSDB; AAX07066.
 XX
 PT New isolated mitogen-activated protein kinase isoforms - used
 PT to develop products for treating e.g. inflammatory disorders,
 PT oxidative damage, proliferative disorders or autoimmune disorders
 XX
 PS Disclosure; Page 129; 168pp; English.
 PS
 CC This polypeptide comprises human mitogen activated protein (MAP)
 CC kinase kinase 6 (MKK6). The amino acid sequence was deduced from an
 CC isolated human skeletal muscle cDNA clone (see AAX07066) and shows
 CC high homology to human MKK3 (see AAM97668). The human MAP kinase
 CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAM97664 and AAM97668-72),
 CC described in the invention, mediate the transduction of specific
 CC signals from the cell surface to the nucleus along specific
 CC pathways. They are useful for screening reagents which modulate
 CC MKK activity. Such agents can be used to prevent or treat
 CC MKK-mediated disorders, e.g. inflammation, oxidative damage or
 CC stress-related proliferative disorders, e.g. psoriasis, AIDS,
 CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,
 CC gastrointestinal system and genito-urinary tract. Agents which
 CC inhibit the activity or expression of MKK inhibit cell growth or
 CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and
 CC polypeptides (see AAM97662-67) are claimed.

XX	Seq	334 AA.	
QY	Query Match	81.9%; Score 1359; DB 20; Length 334;	
Db	Best Local Similarity	82.4%; Pred. No. 1.6e-126;	
QY	Matches 257; Conservative	30; Mismatches 25; Indels 0; Gaps 0;	
QY	5	PAPNPPTPPRNLDLSKRFITTGDRMEFEVADLVLTISLGRGAYGVVEKVRHQAOSGITMAVK	64
Db	23	POTSSTTPRDLDSKSCISIGNONFEVAKDLEPIMLELGAGAVVEKVRHVSQGIIMAVK	82
QY	65	RIRATVNSOEQRLLMDIDINMRTVDCFYTYVFYCALPREGVWIMCMLMDTSLDKFYKQ	124
Db	83	RIRATVNSOEQRLLMDIDISMTVDCPTVFYFALPREGVWIMCMLMDTSLDKFYKQ	142
QY	125	VLDKMTITPEDILGELIAVSIVALEHLHSKLSVIRHDVYKPSVNLINKEGHVWICDFGISG	184
Db	143	VIDKQITIPEDILGLIAVSIVALEHLHSKLSVIRHDVYKPSVNLINALGQVWICDFGISG	202
QY	185	YLVDVSVAATMDAGCKPRYMAPERINELNOKGVNKSVDWLSGITIMELMILIRFPYESNGT	244
Db	203	YLVDVSVAATIDAGCKPRYMAPERINELNOKGVNKSVDWLSGITIMELMILIRFPDYSNGT	262
QY	245	PFQQLKQVVEEBSPOLPADRFSPPEFVDFTAQCLRNKPAERMSYLELMEHPFTLHKTKYT	304
Db	263	PFQQLKQVVEEBSPOLPADRFSAERFVDFTSQCLTKKNSKERPTYPPELMQHPFTLHESKGT	322
QY	305	DIAAFVKILGE	316
Db	323	DVASFVKILIGD	334

RESULT 15
AAY57392

1D	AA193928cancatq; Protein; 334 AA.
XX	
AC	AAV57392;
XX	
DT	19-JUN-2000 (first entry)
DE	Human MAPK kinase 6 polypeptide.
XX	
KW	Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense; sandwich assay; human.
XX	
OS	Homo sapiens.
XX	
PN	US6033910-A.
XX	
PD	07-MAR-2000.
XX	
PF	19-JUL-1999; 99US-0357073.
XX	
PR	19-JUL-1999; 99US-0357073.
XX	
PA	(ISTS-) ISTS PHARM INC.
XX	
PI	Monia BP, Cowseert LM;
XX	
DR	WPI: 2000-269479/23.
DR	N-PSDB; AA298598.
XX	
PT	Novel antisense oligonucleotides used for inhibition of Mitogen-activated protein kinase kinase 6 expression -
XX	
PS	Example 13; Columns 45-50; 33pp; English.
XX	
CC	The invention provides antisense oligonucleotides which are targeted to a nucleic acid encoding a mitogen-activated protein kinase (MAPK) kinase 6.
CC	The antisense oligonucleotides are used to inhibit MAPK kinase 6 expression, and so are used to treat diseases mediated by MAPK kinase 6 expression. They may also be used to detect MAPK kinase 6, e.g. in sandwich assays. The present sequence represents the human MAPK kinase 6.
CC	

XX	Sequence	334 AA:	81.9%; Score 1359; DB 21; Length 334;
QY	Query Match	82.4%; Pred. No. 1,66-126;	
Db	Best Local Similarity	Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0	
QY	5	PAENPTPRNRIDSRFTITGDMPBEVEADLVTISELGRGAYGVVEKVRHMQSGITMAVK	64
Db	23	PQTSTPRDRDYSKACISIGNQNEFVKADDDLEPIELERGAYGVVEKRRHPSPGQIMAVK	82
QY	65	RIRATVNSQEQKRLLMDIDIMMRVTDCYVTTFYGALFREGDWTICMELMTSDLDKPYRK	124
Db	83	RIRATVNSQEQKRLLMDIDIMMRVTDCYVTTFYGALFREGDWTICMELMTSDLDKPYKQ	142
QY	125	VLDKNMTIPEDILGEIAVSIYRALFHLHSKLSVIRHDVQPSNVLLNKEGHVQKCDPFGISG	184
Db	143	VIDKQGITPEIDILGEIAVSIYKALEHLHSKLSVIRHDVQPSNVLLNALGOVMKCDPFGISG	202
QY	185	YLVDVSVAKTMAGCKPYMAPERINPELNLQKGYNSKVDVWSLGITWIEINALIRFPYESWGT	244
Db	203	YLVDVSVAKTIDAGCKPYMAPERINPELNLQKGYNSKVDVWSLGITWIEINALIRFPDWSGT	262
QY	245	PFQOLKQVVEEPPSPOLPADRFSPEFVDFTAOCLRNKPAERNMSYELMEHPFTLHKTKYT	304
Db	263	PFQOLKQVVEEPPSPOLPADRFSPEFVDFTSOCLKNKSKERPTYPPELMQHPFTLHESKGT	322
QY	305	DIAAFVKKILGE 316	
Db	323	DVASFVKLLIGD 334	

Search completed: November 5, 2003, 20:03:48
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: November 5, 2003, 20:03:52 / Search time 22 Seconds
(without alignments)
611.584 Million cell updates/sec

Title: US-09-761-569-2

Perfect score: 1660
Sequence: 1 MSKPPAPNPPTPRNLSRFTF.....HKTGTDIAAFVKILGEDS 318

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1660	100.0	318	1 US-08-530-950-2	Sequence 2, Appl
2	1660	100.0	318	3 US-09-149-879-2	Sequence 2, Appl
3	1660	100.0	318	4 US-09-057-009-2	Sequence 2, Appl
4	1653	99.6	318	3 US-08-888-429A-2	Sequence 2, Appl
5	1644	99.0	318	1 US-08-446-083-2	Sequence 2, Appl
6	1359	81.9	334	1 US-08-530-950-4	Sequence 4, Appl
7	1359	81.9	334	3 US-08-576-240-2	Sequence 4, Appl
8	1359	81.9	334	3 US-08-888-429A-4	Sequence 4, Appl
9	1359	81.9	334	3 US-09-149-879-4	Sequence 4, Appl
10	1359	81.9	334	4 US-09-057-009-4	Sequence 4, Appl
11	946	57.0	185	4 US-09-384-162-11	Sequence 11, Appl
12	888.5	53.5	363	1 US-08-530-950-6	Sequence 6, Appl
13	888.5	53.5	363	3 US-08-888-429A-6	Sequence 6, Appl
14	888.5	53.5	363	3 US-09-149-879-6	Sequence 6, Appl
15	888.5	53.5	363	4 US-09-057-009-6	Sequence 6, Appl
16	888.5	53.5	363	3 US-08-888-429A-8	Sequence 8, Appl
17	888.5	53.5	399	1 US-08-530-950-10	Sequence 10, Appl
18	888.5	53.5	399	2 US-08-874-186-92	Sequence 92, Appl
19	888.5	53.5	399	3 US-08-888-429A-10	Sequence 10, Appl
20	888.5	53.5	399	3 US-09-149-879-10	Sequence 10, Appl
21	888.5	53.5	399	4 US-09-057-009-10	Sequence 10, Appl
22	872.5	52.6	393	1 US-08-530-950-8	Sequence 8, Appl
23	872.5	52.6	393	3 US-09-149-879-8	Sequence 8, Appl
24	872.5	52.6	393	4 US-09-057-009-8	Sequence 8, Appl
25	697	42.0	393	3 US-08-888-429A-21	Sequence 21, Appl
26	697	42.0	487	4 US-09-206-166-6	Sequence 6, Appl
27	670	40.4	419	4 US-09-206-166-2	Sequence 2, Appl

28	670	40.4	435	4 US-09-446-754-2	Sequence 2, Appl
29	664	40.0	389	3 US-08-888-429A-20	Sequence 20, Appl
30	664	40.0	419	3 US-08-888-429A-28	Sequence 28, Appl
31	664	40.0	419	4 US-09-446-754-6	Sequence 6, Appl
32	664	40.0	419	4 US-09-206-166-5	Sequence 5, Appl
33	664	40.0	468	4 US-09-446-754-4	Sequence 4, Appl
34	660.5	39.8	453	3 US-08-888-429A-32	Sequence 32, Appl
35	660	39.8	346	3 US-08-888-429A-18	Sequence 18, Appl
36	657.5	39.6	380	3 US-08-888-429A-30	Sequence 30, Appl
37	657	39.6	468	4 US-09-446-754-10	Sequence 10, Appl
38	586	35.3	367	3 US-08-888-429A-13	Sequence 13, Appl
39	573	34.5	393	1 US-08-423-399B-33	Sequence 33, Appl
40	573	34.5	393	1 US-08-530-950-11	Sequence 11, Appl
41	573	34.5	393	3 US-08-888-429A-11	Sequence 11, Appl
42	573	34.5	393	3 US-09-149-879-11	Sequence 11, Appl
43	573	34.5	393	4 US-09-057-009-11	Sequence 11, Appl
44	570.5	34.4	668	1 US-08-530-950-13	Sequence 13, Appl
45	570.5	34.4	668	3 US-09-149-879-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-530-950-2
; Sequence 2, Application US/08530950
; Patent No. 5736381
; GENERAL INFORMATION:
; APPLICANT: Davila, Roger J.
; APPLICANT: Raingeaud, Joel
; APPLICANT: Gupta, Shashi
; APPLICANT: Derjard, Benoit
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
; TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,950
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07917/010001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; US-08-530-950-2
Query Match 100.0%; Score 1660; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.7e-158;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKPPAPNPPTPRNLSRFTITIGDMFVEADLVITISLGGAGVGVKXHAQSGTI 60

|||||
Db 1 MSKPPANPTPPNLDSTRFTITIGDRMFVEVADLVITISLGGAGVVEKVAHQSGTI 60
Qy 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
Db 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
Qy 121 FFRKVLDDKMTIPEDILGIAVSIVRALBHLHSKLSVIHRDVKPSNVLINKEGHVMGCDP 180
Db 121 FFRKVLDDKMTIPEDILGIAVSIVRALBHLHSKLSVIHRDVKPSNVLINKEGHVMGCDP 180
Qy 181 GISGYLVDVSAKTMADGCKPYMAPERINPELNQKGVNKS DWSLGI TWIEMAILRFPYE 240
Db 181 GISGYLVDVSAKTMADGCKPYMAPERINPELNQKGVNKS DWSLGI TWIEMAILRFPYE 240
Qy 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLETMEHPFTLHK 300
Db 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLETMEHPFTLHK 300
Qy 301 TKKTDIAAFVKKILGEDS 318
Db 301 TKKTDIAAFVKKILGEDS 318

RESULT 2

US-09-149-879-2
Sequence 2, Application US/09149879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Rainsgaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-2

Query Match

100.0%; Score 1660; DB 3; Length 318;

Best Local Similarity 100.0%; Pred. No. 3,7e-158;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKPPANPTPPNLDSTRFTITIGDRMFVEVADLVITISLGGAGVVEKVAHQSGTI 60
Db 1 MSKPPANPTPPNLDSTRFTITIGDRMFVEVADLVITISLGGAGVVEKVAHQSGTI 60
Qy 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
Db 61 MAVKIRATVNSOQKRLMDLDINMRTVDCFTYTFYGLFREGDVMICMELMDTSLDK 120
Qy 121 FFRKVLDDKMTIPEDILGIAVSIVRALBHLHSKLSVIHRDVKPSNVLINKEGHVMGCDP 180
Db 121 FFRKVLDDKMTIPEDILGIAVSIVRALBHLHSKLSVIHRDVKPSNVLINKEGHVMGCDP 180
Qy 181 GISGYLVDVSAKTMADGCKPYMAPERINPELNQKGVNKS DWSLGI TWIEMAILRFPYE 240
Db 181 GISGYLVDVSAKTMADGCKPYMAPERINPELNQKGVNKS DWSLGI TWIEMAILRFPYE 240
Qy 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLETMEHPFTLHK 300
Db 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAOCLRNKPARMSYLETMEHPFTLHK 300
Qy 301 TKKTDIAAFVKKILGEDS 318
Db 301 TKKTDIAAFVKKILGEDS 318

RESULT 3

US-09-057-009-2
Sequence 2, Application US/09057009
Patent No. 6541605
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Rainsgaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,009
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6541605 Relevant

TOPOLOGY: linear
US-09-057-009-2

Query Match 100.0%; Score 1660; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.7e-158;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKPPAPPTPPRNLDSRTFTITIGDRMFEVADLVITSELGRGAYGVKVRHAOSGTI 60
DB 1 MSKPPAPPTPPRNLDSRTFTITIGDRMFEVADLVITSELGRGAYGVKVRHAOSGTI 60
QY 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYGLFREGDVMICMLDTSLDK 120
DB 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYGLFREGDVMICMLDTSLDK 120
QY 121 FYRVLDKNMTIPEDILGEIAVSIVRALEHLSKLSVIHRDVKSNTVINKEGHVKMCD 180
DB 121 FYRVLDKNMTIPEDILGEIAVSIVRALEHLSKLSVIHRDVKSNTVINKEGHVKMCD 180
QY 181 GISGYLVDVAKTMDAGCKPYMAPERINPELNOKGVKSDVMSLGTIMEMALIRPEYE 240
DB 181 GISGYLVDVAKTMDAGCKPYMAPERINPELNOKGVKSDVMSLGTIMEMALIRPEYE 240
QY 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAQCLRKPAERMSTYELMEHPFTLHK 300
DB 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAQCLRKPAERMSTYELMEHPFTLHK 300
QY 301 TKKTIDIAFVKKILGEDS 318
DB 301 TKKTIDIAFVKKILGEDS 318

RESULT 4
US-08-888-429A-2

Sequence 2, Application US/0888429A
Patent No. 6136596

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan

APPLICANT: Tounier, Cathy
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-

TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A

FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995

APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.

REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 299354

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-888-429A-2

Query Match 99.6%; Score 1653; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.9e-157;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPPAPPTPPRNLDSRTFTITIGDRMFEVADLVITSELGRGAYGVKVRHAOSGTI 60
DB 1 MSKPPAPPTPPRNLDSRTFTITIGDRMFEVADLVITSELGRGAYGVKVRHAOSGTI 60
QY 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYGLFREGDVMICMLDTSLDK 120
DB 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTYVTFYGLFREGDVMICMLDTSLDK 120
QY 121 FYRVLDKNMTIPEDILGEIAVSIVRALEHLSKLSVIHRDVKSNTVINKEGHVKMCD 180
DB 121 FYRVLDKNMTIPEDILGEIAVSIVRALEHLSKLSVIHRDVKSNTVINKEGHVKMCD 180
QY 181 GISGYLVDVAKTMDAGCKPYMAPERINPELNOKGVKSDVMSLGTIMEMALIRPEYE 240
DB 181 GISGYLVDVAKTMDAGCKPYMAPERINPELNOKGVKSDVMSLGTIMEMALIRPEYE 240
QY 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAQCLRKPAERMSTYELMEHPFTLHK 300
DB 241 SWGTPFOQLKQVVEEPPQLPADRFSPFVDFTAQCLRKPAERMSTYELMEHPFTLHK 300
QY 301 TKKTIDIAFVKKILGEDS 318
DB 301 TKKTIDIAFVKKILGEDS 318

RESULT 5
US-08-446-083-2

Sequence 2, Application US/08446083
Patent No. 5804427

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
APPLICANT: Raugeaud, Joel

APPLICANT: Gupta, Shashi
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND

TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,083

FILING DATE: 19-MAY-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter

REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/066001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-446-083-2

Query Match 99.0%; Score 1644; DB 1; Length 318;
Best Local Similarity 99.4%; Pred. No. 1,5e-156;
Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSKPPAPNPTRPRLDRTFTTIGDRMFEVADDLVTISLGGAGVGEKVAHAGSTI 60
DB 1 MSKPPAPNPTRPRLDRTFTTIGDRMFEVADDLVTISLGGAGVGEKVAHAGSTI 60
QY 61 MAVKRIATVNSGQKRLMDLDINMRTVDCFTYVTFYGLAFREGDVMICMELMDTSLDK 120
DB 61 MAVKRIATVNSGQKRLMDLDINMRTVDCFTYVTFYGLAFREGDVMICMELMDTSLDK 120
QY 121 FYRKVLDKNMTIPEDILGEIATVIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDP 180
DB 121 FYRKVLDKNMTIPEDILGEIATVIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDP 180
QY 181 GISGYLVDSVAKTMDACCKPYMAPERINPELNOKGVNSDWSLGTMTIEMALIRPEYE 240
DB 181 GISGYLVDSVAKTMDACCKPYMAPERINPELNOKGVNSDWSLGTMTIEMALIRPEYE 240
QY 241 SWGTFPQQLKQVVEEPPQLPADRFSPFVDFYTAOCLRKXNPAERMSYLEMEHPFTLHK 300
DB 241 SWGTFPQQLKQVVEEPPQLPADRFSPFVDFYTAOCLRKXNPAERMSYLEMEHPFTLHK 300
QY 301 TKKTIDIAAFVKXILGEDS 318
DB 301 TKKTIDIAAFVKXILGEDS 318

RESULT 6
US-08-530-950-4
Sequence 4, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Ralingeand, Josei
APPLICANT: Gupta, Shaehi
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530.950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-4

Query Match 81.9%; Score 1359; DB 1; Length 334;
Best Local Similarity 82.4%; Pred. No. 5,5e-128;
Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

QY 5 PAPNPTRPRLDRTFTTIGDRMFEVADDLVTISLGGAGVGEKVAHAGSTI 64
DB 23 PQTSTPPRLDLSKACISIGNONFEVKADDELPIMELGGAAGVGEKVAHAGSTI 82
QY 65 RIRATVNSGQKRLMDLDINMRTVDCFTYVTFYGLAFREGDVMICMELMDTSLDKFYRK 124
DB 83 RIRATVNSGQKRLMDLDINMRTVDCFTYVTFYGLAFREGDVMICMELMDTSLDKFYRK 142
QY 125 VIDKNTIPEDILGEIATVIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDPFGISG 184
DB 143 VIDKNTIPEDILGEIATVIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDPFGISG 202
QY 185 YLVDSVAKTMDACCKPYMAPERINPELNOKGVNSDWSLGTMTIEMALIRPEYESMT 244
DB 203 YLVDSVAKTMDACCKPYMAPERINPELNOKGVNSDWSLGTMTIEMALIRPEYESMT 262
QY 245 PFOQLKQVVEEPPQLPADRFSPFVDFYTAOCLRKXNPAERMSYLEMEHPFTLHKTKT 304
DB 263 PFOQLKQVVEEPPQLPADRFSPFVDFYTAOCLRKXNPAERMSYLEMEHPFTLHKTKT 322
QY 305 DIAAFVKXILGE 316
DB 323 DVASFVKXILGD 334

RESULT 7
US-08-576-240-2
Sequence 2, Application US/08576240
Patent No. 6074862
GENERAL INFORMATION:
APPLICANT: Stein, Bernd
APPLICANT: Yang, Maria
TITLE OF INVENTION: MITOGEN-ACTIVATED PROTEIN KINASE
TITLE OF INVENTION: MEKE AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,240
FILING DATE: 20-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098, 403
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:

Qy 35 LVITSELGARGAVGEKVRHQAOSGTINAVKIRATVNSOEQRLLMDLIMRTVDFEYT 94
 Db 1 LVITSELGARGAVGEKVRHQAOSGTINAVKIRATVNSOEQRLLMDLIMRTVDFEYT 60
 Qy 95 VTFPGALFRBGDWCIMELNDTSIDKRYKVLNDKMTIPEDICEIAVSIVRALEHLHSK 154
 Db 61 VTFPGALFRBGDWCIMELNDTSIDKRYKVLNDKMTIPEDICEIAVSIVRALEHLHSK 96
 Qy 155 LSVHRVQKPSNVNINKGHVQKMGDPGSGYLVDSVAKTMDAGCKPYMAPERINPELNOK 214
 Db 97 LSVHRVQKPSNVNINKGHVQKMGDPGSGYLVDSVAKTMDAGCKPYMAPERINPELNOK 156
 Qy 215 GYNVKSQVWSLIGITMIEMALRFPYESWG 243
 Db 157 GYNVKSQVWSLIGITMIEMALRFPYESWG 185

RESULT 12
 US-08-530-950-6
 ; Sequence 6, Application US/08530950
 ; Patent No. 5736381
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Roger J.
 ; APPLICANT: Raingeaud, Joel
 ; APPLICANT: Gupta, Shashi
 ; APPLICANT: Derjard, Benoit
 ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
 ; TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/530,950
 ; FILING DATE: 19-SEP-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07917/010001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; US-08-530-950-6

Query Match 53.5%; Score 888.5; DB 1; Length 363;
 Best Local Similarity 52.6%; Pred. No. 8.2e-81;
 Matches 172; Conservative 60; Mismatches 76; Indels 19; Gaps 5;

Qy 7 PNPTPPN-----LDSRTFITG-DRMFEVADDLVITSELGARGAVGEKVRHQA 55
 Db 27 PNPTGVNPHIERLRTHTSISSGKLTSPQHMDFTAEDLKDGEIGRGAVGVNKNVHK 86
 Qy 56 QSGTINAVKIRATVNSOEQRLLMDLIMRTVDFEYTTFYGLAFRBDWCIMELND 115
 Db 87 PSGQINAVKIRATVNSOEQRLLMDLIMRTVDFEYTTFYGLAFRBDWCIMELNS 146

Qy 116 TSLDKFYR---KYLDKNMTIPEDICEIAVSIVRALEHLHSKLSVHRVQKPSNVNINK 172
 Db 147 TSLDKFYRYVSLDD--VPEELIGKITATYALNHLKENTKIHRDKPSVILDRS 204
 Qy 173 GHVQKMGDPGSGYLVDSVAKTMDAGCKPYMAPERINPELNOKGYNVKSQVWSLIGITMIEM 232
 Db 205 GNIKLOPFGISGQLVDSIAKTRDAGCKPYMAPERIDPSASRQGYDVASDVWSLIGITLYEL 264
 Qy 233 AILRFPYESWGTPQQLKQVVEBSPQLPAD--RSPPEVDFTAOCLRNKPAERMSYLE 289
 Db 265 ATRGFPPKWNVSVEFDLTQVVKGDPQLNSSEEREFSPFINFVNLCITRDESKRPYKE 324
 Qy 290 LMEHPFTLHKTCTDIAFAVKKIIGE 316
 Db 325 LKHPFLMYERAEVACVCKILDO 351

RESULT 13
 US-08-888-429A-6
 ; Sequence 6, Application US/08888429A
 ; Patent No. 6136596
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Roger J.
 ; APPLICANT: Whitmarsh, Alan
 ; APPLICANT: Tournier, Cathy
 ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
 ; TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/888,429A
 ; FILING DATE: 07-JUL-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/530,950
 ; FILING DATE: 19-SEP-1995
 ; APPLICATION NUMBER: 08/446,083
 ; FILING DATE: 19-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, Peter J.
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07917/053001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 299354
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 363 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-888-429A-6

Query Match 53.5%; Score 888.5; DB 3; Length 363;
 Best Local Similarity 52.6%; Pred. No. 8.2e-81;
 Matches 172; Conservative 60; Mismatches 76; Indels 19; Gaps 5;

Qy 7 PNPTPPN-----LDSRTFITG-DRMFEVADDLVITSELGARGAVGEKVRHQA 55
 Db 27 PNPTGVNPHIERLRTHTSISSGKLTSPQHMDFTAEDLKDGEIGRGAVGVNKNVHK 86

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 20:04:52 : Search time 42 seconds
(without alignments)
1300.387 Million cell updates/sec

Title: US-09-761-569-2

Perfect score: 1660
Sequence: 1 MSKPPAPNPTRPRLDSTRF.....HKTCKTIDIAFVKILGEDS 318

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1660	100.0	318	10	US-09-761-569-2
2	1653	99.6	318	11	US-09-981-397A-20
3	1653	99.6	318	15	US-10-059-585-36
4	1653	99.6	318	16	US-10-137-953-2
5	1359	81.9	333	12	US-10-406-730-2
6	1359	81.9	334	10	US-09-761-569-4
7	1359	81.9	334	16	US-10-137-953-4
8	888.5	53.5	363	16	US-09-761-569-6
9	888.5	53.5	363	16	US-10-137-953-8
10	888.5	53.5	399	10	US-10-137-953-10
11	888.5	53.5	399	15	US-09-761-569-10
12	888.5	53.5	399	15	US-10-288-222A-8
13	888.5	53.5	399	16	US-10-137-953-10
14	872.5	52.6	393	10	US-09-761-569-8
15	697	42.0	393	16	US-10-137-953-21

16	668	40.2	419	12	US-10-204-041-6	Sequence 6, Appl1
17	664	40.0	389	16	US-10-137-953-20	Sequence 20, Appl1
18	664	40.0	419	16	US-10-137-953-28	Sequence 28, Appl1
19	660.5	39.8	453	16	US-10-137-953-32	Sequence 32, Appl1
20	660	39.8	346	16	US-10-137-953-18	Sequence 18, Appl1
21	657.5	39.6	380	16	US-10-137-953-30	Sequence 30, Appl1
22	586	35.3	367	16	US-10-137-953-13	Sequence 13, Appl1
23	573	34.5	389	10	US-09-755-665-36	Sequence 36, Appl1
24	573	34.5	393	10	US-09-761-569-11	Sequence 11, Appl1
25	573	34.5	393	11	US-09-918-873-4	Sequence 4, Appl1
26	573	34.5	393	16	US-10-137-953-11	Sequence 11, Appl1
27	572.5	34.5	600	15	US-10-128-714-3202	Sequence 3202, Ap
28	572.5	34.5	656	15	US-10-128-714-8202	Sequence 8202, Ap
29	570.5	34.4	668	10	US-09-761-569-13	Sequence 13, Appl1
30	570.5	34.4	668	10	US-09-801-368-238	Sequence 238, App
31	570.5	34.4	668	15	US-10-081-119-20	Sequence 20, Appl1
32	566	34.1	400	10	US-09-761-569-12	Sequence 12, Appl1
33	565.5	34.1	545	12	US-10-032-585-7762	Sequence 7762, Ap
34	565	34.0	395	10	US-09-755-665-34	Sequence 34, Appl1
35	565	34.0	400	16	US-10-137-953-12	Sequence 12, Appl1
36	564	34.0	400	12	US-09-769-970-17	Sequence 17, Appl1
37	560	33.7	400	12	US-09-769-970-3	Sequence 3, Appl1
38	550.5	33.2	359	12	US-10-159-971A-4	Sequence 4, Appl1
39	550.5	33.2	405	16	US-10-137-953-22	Sequence 22, Appl1
40	550.5	33.2	448	12	US-10-159-971A-1	Sequence 1, Appl1
41	539	32.5	364	10	US-09-755-665-64	Sequence 64, Appl1
42	531	32.0	392	10	US-09-755-665-35	Sequence 35, Appl1
43	531	32.0	394	10	US-09-755-665-33	Sequence 33, Appl1
44	519	31.3	380	10	US-09-755-665-8	Sequence 8, Appl1
45	495	29.8	369	10	US-09-755-665-16	Sequence 16, Appl1

ALIGNMENTS

RESULT 1
US-09-761-569-2
Sequence 2, Application US/09761569
Patent No. US20020102691A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Gupta, Shaeshi
Derjard, Benoit
TITLE OF INVENTION: CYTOKINE, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,569
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,009
FILING DATE: 1998-04-07
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020102691A1 Relevant
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-761-569-2

Query Match 100.0%; Score 1660; DB 10; Length 318;
Best Local Similarity 100.0%; Pred. No. 9.3e-149;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60
DB 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60
QY 61 MAVKRIRATVNSQEQKRLMDLDINMRTVDCFTYTFYGALFREGDVMICMELMDTSLDK 120
DB 61 MAVKRIRATVNSQEQKRLMDLDINMRTVDCFTYTFYGALFREGDVMICMELMDTSLDK 120
QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHLSKLSVIRHDVPSNVLINKEGHVKMGCF 180
DB 121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHLSKLSVIRHDVPSNVLINKEGHVKMGCF 180
QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNSDVMSLGTIEMAILRFPYE 240
DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNSDVMSLGTIEMAILRFPYE 240
QY 241 SWGTPFOQLKQVVEEBSPOLPADRFSPFVDTAOCIRNPAERMSYLELMEHPFTTLHK 300
DB 241 SWGTPFOQLKQVVEEBSPOLPADRFSPFVDTAOCIRNPAERMSYLELMEHPFTTLHK 300
QY 301 TKKTIDIAFVKKILGEDS 318
DB 301 TKKTIDIAFVKKILGEDS 318

RESULT 2
US-09-981-397A-20
Sequence 20, Application US/09981397A
Publication No. US20030082519A1
GENERAL INFORMATION:
APPLICANT: Axixma Pharmaceuticals AG
APPLICANT: Schubart, Daniel
APPLICANT: Habenberger, Peter
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
FILE REFERENCE: AXM-004.1 US
CURRENT APPLICATION NUMBER: US/09/981.397A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/240,750
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-981-397A-20

Query Match 99.6%; Score 1653; DB 11; Length 318;
Best Local Similarity 99.7%; Pred. No. 4.3e-148;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60
DB 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60

QY 61 MAVKRIRATVNSQEQKRLMDLDINMRTVDCFTYTFYGALFREGDVMICMELMDTSLDK 120
DB 61 MAVKRIRATVNSQEQKRLMDLDINMRTVDCFTYTFYGALFREGDVMICMELMDTSLDK 120
QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHLSKLSVIRHDVPSNVLINKEGHVKMGCF 180
DB 121 FYRKVLDKNMTIPEDILGEIAVSIVRALEHLHLSKLSVIRHDVPSNVLINKEGHVKMGCF 180
QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNSDVMSLGTIEMAILRFPYE 240
DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNSDVMSLGTIEMAILRFPYE 240
QY 241 SWGTPFOQLKQVVEEBSPOLPADRFSPFVDTAOCIRNPAERMSYLELMEHPFTTLHK 300
DB 241 SWGTPFOQLKQVVEEBSPOLPADRFSPFVDTAOCIRNPAERMSYLELMEHPFTTLHK 300
QY 301 TKKTIDIAFVKKILGEDS 318
DB 301 TKKTIDIAFVKKILGEDS 318

RESULT 3
US-10-059-585-36
Sequence 36, Application US/10059585
Publication No. US2003008276A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsuji
APPLICANT: Funahashi, Shin-ichi
APPLICANT: Senoo, Chiaki
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
FILE REFERENCE: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-059-585-36

Query Match 99.6%; Score 1653; DB 15; Length 318;
Best Local Similarity 99.7%; Pred. No. 4.3e-148;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60
DB 1 MSKPPAPNPPTPPRNLDSTRTITIGDRMFVEADDLVTISLGRGAGVVEKVRHAOSGTT 60

QY 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDK 120
 DB 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDK 120
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDF 180
 DB 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDF 180
 QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYE 240
 DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYE 240
 QY 241 SWGTPFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHK 300
 DB 241 SWGTPFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHK 300
 QY 301 TKKTDIAAFVKKILGEDS 318
 DB 301 TKKTDIAAFVKKILGEDS 318

RESULT 4

US-10-137-953-2
 ; Sequence 2, Application US/10137953
 ; Publication No. US20030129606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Roger J.
 ; Whitmarsh, Alan
 ; Tournier, Cathy
 ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
 ; ACTIVATED HUMAN PROTEIN KINASE KINASES
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P. C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/137,953
 ; FILING DATE: 03-May-2002
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/888,429
 ; FILING DATE: 07-JUL-1997
 ; APPLICATION NUMBER: 08/530,950
 ; FILING DATE: 19-SEP-1995
 ; APPLICATION NUMBER: 08/446,083
 ; FILING DATE: 19-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paege, Peter J.
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07917/005001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 299354
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 318 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-137-953-2

Query Match 99.6%; Score 1653; DB 16; Length 318;

Best Local Similarity 99.7%; Pred. No. 4,3e-148;
 Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSKPPAPNPPTPRNLDRTITTTGDRMFEVADDLVITISLGRGAYGVKVRHAQSGTI 60
 DB 1 MSKPPAPNPPTPRNLDRTITTTGDRMFEVADDLVITISLGRGAYGVKVRHAQSGTI 60
 QY 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDK 120
 DB 61 MAVRIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDK 120
 QY 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDF 180
 DB 121 FYRKVLDKNMTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDF 180
 QY 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYE 240
 DB 181 GISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYE 240
 QY 241 SWGTPFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHK 300
 DB 241 SWGTPFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHK 300
 QY 301 TKKTDIAAFVKKILGEDS 318
 DB 301 TKKTDIAAFVKKILGEDS 318

RESULT 5

US-10-406-730-2
 ; Sequence 2, Application US/10406730
 ; Publication No. US20030175928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinh, Bernd
 ; Applicant: Yang, Maria X. H.
 ; TITLE OF INVENTION: MITOGEN-ACTIVATED PROTEIN KINASE KINASE
 ; TITLE OF INVENTION: MEK6 AND METHODS OF USE THEREFOR
 ; FILE REFERENCE: 860098.403CI
 ; CURRENT APPLICATION NUMBER: US/10/406,730
 ; CURRENT FILING DATE: 2003-04-02
 ; PRIOR APPLICATION NUMBER: US/09/593,288
 ; PRIOR FILING DATE: 2000-06-12
 ; PRIOR APPLICATION NUMBER: US 08/576,240
 ; PRIOR FILING DATE: 1995-12-20
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 333
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 ; US-10-406-730-2

Query Match 81.9%; Score 1359; DB 12; Length 333;
 Best Local Similarity 82.4%; Pred. No. 3e-120;
 Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

QY 5 PARNPPRRRLDRTFTITTDKRMFEVADDLVITISLGRGAYGVKVRHAQSGTI 64
 DB 5 PARNPPRRRLDRTFTITTDKRMFEVADDLVITISLGRGAYGVKVRHAQSGTI 64
 QY 22 PQSTSPRRDLDRKACISIGNQNFVYADDLLEIMEGRAYGVKVRHAQSGTI 81
 DB 22 PQSTSPRRDLDRKACISIGNQNFVYADDLLEIMEGRAYGVKVRHAQSGTI 81
 QY 65 RIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDKFYRK 124
 DB 65 RIRATVNSOQKRLMDLDINMRTVDCFTVTYFGALFREGDVMICMELMDTSLDKFYRK 124
 QY 125 VLDKNTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDFISIG 184
 DB 125 VLDKNTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDFISIG 184
 QY 142 VIDKGTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDFISIG 201
 DB 142 VIDKGTIPEDILGEIAVSIVRALHLSKLSVIHRDVKPSNVLINKEGVKXKCDFISIG 201
 QY 185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYEWGT 244
 DB 185 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYEWGT 244
 QY 202 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYEWGT 261
 DB 202 YLVDSVAKTMDAGCKPYMAPERINPELNQKGVNKSVDVSLGTTMELMILRPEYEWGT 261
 QY 245 PFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHKTKYT 304
 DB 245 PFOQLKQVVEEBSPOLPADRFSPPEVDFTACLRKPAERMSYLELMEHPFTLHKTKYT 304

Db 262 PFQOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNKSKERPTPELMQHFFTLHESKGT 321

QY 305 DIAAFVKILGE 316
Db 322 DVASFVKILIGD 333

RESULT 6

US-09-761-569-4
Sequence 4, Application US/09761569
Patent No. US20020102691A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
Ratigeaud, Joel
Gupta, Shaash
Derlward, Benoit

TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761,569

FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,009

FILING DATE: 1998-04-07

ATTORNEY/AGENT INFORMATION:

NAME: Faase, J. Peter

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 07911/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 334 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20020102691A1 Relevant

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-761-569-4

Query Match 81.9%; Score 1359; DB 10; Length 334;

Best Local Similarity 82.4%; Pred. No. 3e-120;

Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

Db 5 PARNPPRNLDSRTFTTIGDRMFEVADLVITSELGAGAYGVVEKRAHAAOSGTTMAVK 64

QY 23 PQTSTTPRDLSDACISIGNONFEVKADDLPEIMELGAGAYGVVEKRAHAAOSGTTMAVK 82

Db 65 RIRATVNSQEQKRLMDLDMNRTVDCFTYTFYFGLFREGDVIICMELMDTSLDKFYRK 124

QY 83 RIRATVNSQEQKRLMDLDMNRTVDCFTYTFYFGLFREGDVIICMELMDTSLDKFYRK 142

Db 125 VLDKMTIPEDILGELAVSIVRALEHLHSLKSLVIRHDKPSNVLINKEGVKKKCDGIGS 184

QY 143 VIDKGTIPEDILGELAVSIVRALEHLHSLKSLVIRHDKPSNVLINKEGVKKKCDGIGS 202

QY 185 YLVDSVAKTMDAGCKPYMAPERINPELNOKGYVXKSDVMSLGITIMEALRFPYESGCT 244

Db 203 YLVDSVAKTMDAGCKPYMAPERINPELNOKGYVXKSDVMSLGITIMEALRFPYESGCT 262

QY 245 PFQOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNKSKERPTPELMQHFFTLHESKGT 304

Db 263 PFQOLKQVVEEPPQLPADKFSAEFVDFTSQCLKKNKSKERPTPELMQHFFTLHESKGT 322

QY 305 DIAAFVKILGE 316

Db 322 DVASFVKILIGD 334

RESULT 7

US-10-137-953-4

Sequence 4, Application US/10137953
Publication No. US20030129606A1

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
Whitmarsh, Alan

Tournier, Cathy

TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
ACTIVATED HUMAN PROTEIN KINASE KINASES

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/137,953

FILING DATE: 03-May-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/888,429

FILING DATE: 07-JUL-1997

APPLICATION NUMBER: 08/530,950

FILING DATE: 19-SEP-1995

APPLICATION NUMBER: 08/446,083

FILING DATE: 19-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Faase, Peter J.

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 07917/053001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 299354

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 334 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-137-953-4

Query Match 81.9%; Score 1359; DB 16; Length 334;

Best Local Similarity 82.4%; Pred. No. 3e-120;

Matches 257; Conservative 30; Mismatches 25; Indels 0; Gaps 0;

Db 5 PARNPPRNLDSRTFTTIGDRMFEVADLVITSELGAGAYGVVEKRAHAAOSGTTMAVK 64

QY 23 PQTSTTPRDLSDACISIGNONFEVKADDLPEIMELGAGAYGVVEKRAHAAOSGTTMAVK 82

Db 65 RIRATVNSQEQKRLMDLDMNRTVDCFTYTFYFGLFREGDVIICMELMDTSLDKFYRK 124

QY 83 RIRATVNSQEQKRLMDLDMNRTVDCFTYTFYFGLFREGDVIICMELMDTSLDKFYRK 142

Db 125 VLDKMTIPEDILGELAVSIVRALEHLHSLKSLVIRHDKPSNVLINKEGVKKKCDGIGS 184

QY 143 VIDKGTIPEDILGELAVSIVRALEHLHSLKSLVIRHDKPSNVLINKEGVKKKCDGIGS 202

Db 83 RIRATVNSOEOGRLLMDLIDISMRITVDCFTVTFYGALEFRBGDVMICWELMDTSLDKFYKQ 142
Qy 125 VLDKMTIPEDILGEIANSYIRALEHLSKLSVHRDVKPSNVILNKGHVKMCDPFGISG 184
Db 143 VIDGGQITPEIDILKIVSIKALEHLSKLSVHRDVKPSNVILNKGHVKMCDPFGISG 202
Qy 185 YLVDSVAKTMDAGCKPYMAPERINPELNOKGYNSVSLGIMTIEMLIRFPYESMGT 244
Db 203 YLVDSVAKTMDAGCKPYMAPERINPELNOKGYNSVSLGIMTIEMLIRFPYESMGT 262
Qy 245 PFOOLKQVVEEPPSPQLPADRFSPFVDFTQAQCLRNPAERMSYLEMHEPFTLHKTXT 304
Db 263 PFOOLKQVVEEPPSPQLPADRFSAEFVDFTSQCLKNGSKERPTPELMQHPFTLHESKGT 322
Qy 305 DIAAFVKILGE 316
Db 323 DVASFVKILGD 334

RESULT 8

US-09-761-569-6
Sequence 6, Application US/09761569
Patent No. US20020102691A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Raingeaud, Joel
Gupta, Shashi
Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/761,569
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,009
FILING DATE: 1998-04-07
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020102691A1 Relevant
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-761-569-6

Query Match 53.5%; Score 888.5; DB 10; Length 363;
Best Local Similarity 52.6%; Pred. No. 1.le-75;
Matches 172; Conservative 60; Mismatches 76; Indels 19; Gaps 5;

Qy 7 PNPTPPRN-----LDRTFTITG-DRMEFEVADLVITSELGRGAVVEKYRHA 55
Db 27 PNFPGVGNPIHERLIRTHSISSGKLKISPPQHMDFTHEDLKDCEIRGAVGYNKRVKH 86
Qy 56 QSGTINAVKIRATVNSOEOGRLLMDLIDIMKRTVDCFTVTFYGALEFRBGDVMICWELMD 115
Db 87 PSGQIMAVKIRISTVDEKEQQLMDLDVVMRSSDCYIVQFYGALEFRBGDVMICWELMS 146
Qy 116 TSLDKFYR---KVLDMKMTIPEDILGEIANSYIRALEHLSKLSVHRDVKPSNVILNKE 172
Db 147 TSFDKFKYKYVSLDD--VPEELIGKITATAYKALNHLKENLKIHRDIKPSNILLDRS 204
Qy 173 GHVAMCDPFGISGLVDSVAKTMDAGCKPYMAPERINPELNOKGYNSVSLGIMTIEML 232
Db 205 GNILKCDPFGISGLVDSVAKTMDAGCKPYMAPERIDPSASRQGVDSVMSLGITLHYEL 264
Qy 233 AILRFYESWGTFFOOLKQVVEEPPSPQLPAD--RSPFVDFTAQCLRNPAERMSYLE 289
Db 265 ATGRFPYPKWNSVFDQLTVVKGDPQLNSSEEREFSPFINFVNLCTLDESRRPKYKE 324
Qy 290 LMEHPFTLHKTXTDIAAFVKILGE 316
Db 325 LKHPFTLMEYERAVEVACVCKILDO 351

RESULT 9

US-10-137-953-6
Sequence 6, Application US/10137953
Publication No. US20030129606A1
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
Whitmarsh, Alan
Tournier, Cathy
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137,953
FILING DATE: 03-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429
FILING DATE: 07-JUL-1997
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION:	SEQ ID NO:
US-10-137-953-6	6:

Query Match	53.5%	Score 888.5	DB 16	Length 363
Best Local Similarity	53.6%	Pred. No. 1.1e-75		
Matches 172	Conservative 60	Mismatches 76	Indels 19	Gaps 5

[illegible]

RESULT 10
US-10-137-953-8

; Sequence 8, Application US/10137953
; Publication No. US20030129606A1
; GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
Whitmarsh, Alan
Tournier, Cathy

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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM: ;

```

1      MEDIUM TYPE: Diskette
2      COMPUTER: IBM Compatible
3      OPERATING SYSTEM: Windows95
4      SOFTWARE: PackISO for Windows Version 2.0
5
6      CURRENT APPLICATION DATA:
7
8      APPLICATION NUMBER: US/10/137.953
9      FILING DATE: 03-May-2002

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US/08/888,
3 FILING DATE: 07-JUL-1997
4 APPLICATION NUMBER: 08/530,955
5 FILING DATE: 19-SEP-1995
6 APPLICATION NUMBER: 08/446,083
7 FILING DATE: 19-MAY-1995
8 ATTORNEY/AGENT INFORMATION:

```

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS

```

```

; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PROTEIN TYPE:

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;          SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-137-953-8

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Query Match	53.5%;	Score 888.5;	DB 16;	Length 393;
Best Local Similarity	52.6%;	Pred. No. 1.2e-75;		
Matches 172;	Conservative 60;	Mismatches 76;	Indels 19;	Gaps 57;

QY	7	PNDTPERN-----LDSTFTTIG--DMFEVYEDDLVTIIEELRGAYGVVEKVRHA	55
Dd	57	PNPTVGQNHIERLRLTHSISSGKTAKISPEQHMPFTMEDLKDGLGEIRGAVGSNNKVHK	116
QY	56	QSQTIAVKRIPATYNSEOQRLLMMDLDINMTYDCFYTTFFYCALFREBDWIMCHEMD	115
Dd	117	PSQOIMAVKRISTYDEKEOKQLMMDLDVWRSSDCPIYQFYGALFEREDCWMCHELMS	176
QY	116	TSLDKPYR---VLDKNMTTIPEDIAGEIVASIVALEHLSKSLSVHRDPKSPSVLINKE	172
Dd	177	TSDPKRYKKVYSVLDD--VIBEILIGKITTLATAVALNHLKENLIKIHREDIKPNSILLDRS	234
QY	173	GHWKMCDFEISGYLYDSIAKTMNDAGCKEPYMAPESINBELNOKGYNKSDVWSIGITMIEM	232
Dd	235	GNIKCDPFISQOLVDISIAKTRDAGCRPYMAPERIDISASAOGDVSDVWSIGITLYEL	294
QY	233	AIIREFYESWGPFOOLQOVEESPQJLPAD---RFSEFVDFYAQCRLRKPAERMSYLE	289
Dd	295	ATGRFPYPKMNSVFPOQLVOVWKGPDPOLSNEEREFSFINFNULULTDDESRRPRKYE	354
QY	290	LMEHPFTLIHKTXTDIDIAAFVKILIGE	316
Dd	355	LKHGPFILMYERRAWEVACVCKLLDQ	381

RESULT 11
US-09-761-569-10

```

; sequence ID, Application US/09/61563
; Patent No. US20020102691A1
; GENERAL INFORMATION:

```

APPLICANT: Davis, Roger J.
; Raingeaud, Joel
; Gupta, Shashi
;

Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
KINASES

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3d
CURRENT APPLICATION DATA:

```

?      REGISTRATION NUMBER: 32,983
?      REFERENCE/POCKET NUMBER: 07917/010001
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 617/542-5070
?      TELEFAX: 617/542-8906
?      TELEX: 200154
?      INFORMATION FOR SEQ ID NO: 10:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 399 amino acids
?      TYPE: amino acid
?      STRANDNESS: NO. US20020102691A1 Relevant
?      TOPOLOGY: linear
?      SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-761-569-10

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Query Match	53.5%;	Score 888.5;	DB 10;	Length 399;
Best Local Similarity	52.6%;	Pred: No. 1.2e-75;		
Matches 172;	Conservative	60;	Mismatches 76;	Indels 19;
				Gaps 5

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OY 7 NNPTRPRN-----LDSRTFPIIG-DRMEVEVADDLVITSEIGRAGYVEKRYRA 55
Db 63 PNPFTQVNPDHIERLRTHTSISSGKKLISPEQHMDFAEEDLKOLGEIGRAGYSSVNNQVHK 122
OY 56 OSGITMAVYRIRATYNSOEQRKLLMDLDINMRTVDCFYTVTFGALFRSGDWIMCHELMD 115
Db 123 PSGQIMAVYRIRISTYDEKQKQLMDLDVNMSSDDCPYIVQFGALFRSGDCWIMCHELMS 182
OY 116 TSLDKFYR--RYLDPKNMTIPEDILGEIAVSIYRALEHSHSKLSYVHRVQKPSNVLINKE 172
Db 183 TSFDFKFKYVAVSLD--VIPLEIGKITLAFKALNHLKEMNKLIHRIIKPENILLDS 240
OY 173 GHVKKCDPGISGYLVDVAKTMDAGCKFPMAPRINPELNOQGYNKSXYWSIGITMIEM 232
Db 241 GNKIKCDPDISQOLVDSIAKTRDAGCRPMAPRIPDISASRQGYDVRSDWISGITLYEL 300
OY 233 AILRPFYWSYGTPFOOLKQVNEEPPQTLAD--RPSPEFVDTFAOCLKRNPAIMSYLE 289
Db 301 ATGRPFYPRKNSVFDQLTGVVKGDPQLNSNEERESPFINVNLCLTKRDESKRPKYE 360
OY 290 LMEHPEFTLHKTKTDIAFVKKILGE 316
Db 361 LKHPFILLMYERBAVEAVACYCCKILQ 387

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RESULT 12
US-10-288-222A-8
; Sequence 8, Application US/10288222A
; Publication No. US20030119742X1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Galvin, Katherine
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: Methods and Compositions to treat
; TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414
; TITLE OF INVENTION: 10183, 10530, 12680, 17921, 32248, 60489 OR 93804
; FILE REFERENCE: MP12001-286PIR (M)
; CURRENT APPLICATION NUMBER: US/10/288, 222A
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-288-222A-8

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Query March	53.5%	Score 888.5	DB 15	Length 399
Best Local Similarity	52.6%	Pred. No. 1.2e-75		
Matches 172	Conservative 60	Mismatches 76	Indels 19	Gaps 5
QY	7	PNPFPNPRN-----LDSPRTFTTG-DKMEFVEADDDVTIISLGRGAYGVVEKRRHA	55	
DB	63	PNPFTVNPNHRLRLTHSTIESSGKRIKISQCHMDTAEDLKDLGELGRGAYGVSNKMYHK	122	

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0Y      56  OSGITMAVKRIATATNSOEOKRLMDLDMJMTAVDCFFYTFYFGALFREDGVAICMELMD  115
Db      123  PSCGIMAKYKRIKIRSTYDEKEQKOLLMDLDVWMSSDCPYIVQFYGALFREDCMICHELMS  162

0Y      116  TSLDEKFR--KVLDMNTIPEDDIGETAVSIVRALHEHLHSKLSVTHRDVKSNTLINKE  172
Db      183  TSFDKFFKYXVSVLDD--VIPREIIIGKITLATAVKALNHLEKNKLIITHRIDKPSNIIILDS  240

0Y      173  GHVKKDCRGISGLYDVSVAKTMADACKPMAPEINPELNOKGVANKSDVWSIGITMIEM  232
Db      241  GNIKDCDGIISQOLVDSIAKTRDAGCRPMAFERIDPSASRQGYDVKSDVWSIGITILYEL  3000

0Y      233  AILRPYESWGTFRFOOLKQVVEBPSPOLPAD--RSPBFDVFTAOCLRNKPAERMSYLE  289
Db      301  ATGRPPRYPKMNSVFDQLTQVWKGDPQLSNSSEEREPSPSFINFVNCLITKDESKRPKYKE  3600

0Y      290  LMEHPFLLHKTKKTDIAAFVYKKIIGE  316
Db      361  LTKRPFILMYTERAVAVACVYCKILDQ  387

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RESULT 13
 US-10-137-953-10
 ; Sequence 10, Application US/10137953
 ; Publication No. US20030129606a1
 GENERAL INFORMATION:
 APPLICANT: Davis, Roger J.
 Whitmarsh, Alan
 Tournier, Cathy
 TITLE OF INVENTION: CYCOKINE-, STRESS-, AND ONCOPROTEIN-
 ACTIVATED HUMAN PROTEIN KINASE KINASES
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: PASCSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/137,953
 FILING DATE: 03-MAY-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/888,429
 FILING DATE: 07-JUL-1997
 APPLICATION NUMBER: 08/530,950
 FILING DATE: 19-SEP-1995
 APPLICATION NUMBER: 08/446,083
 FILING DATE: 19-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, Peter J.
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07917/053001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 299354
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-137-953-10

Query Match	53.5%	Score 888.5;	DB 16;	length 399;
Best Local Similarity	52.6%;	Pred. No. 1.2e-75;		
Matches 172;	Conservative 60;	Mismatches 76;	Indels 19;	Gaps 5;

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Qy 7 PNPTPPNN-----LDSRTFIIJ -DRFEEVADLDVTI5BLGGAIVGEKRRHA 55
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 63 PNPTGVONPHIEHLRTHSISSGKLI5PQCHMDTAEDLKDLDGEIGRAVG5NNKVHK 122
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 56 QSGTINAVKRIRATVNSOEBKRLMLDLINMTVD0CFYTVTFYGALEPREGDWIMELMD 115
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 123 P5GQINAVKRIRSTVDKEKQKOLMDLDVVMSSPCPIYQFYGALPREGCWI0MELMS 182
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 116 TSLDKFYR---KVLDXNMTIPEDIIIGELAV5IVRLEHLH5KLSVIRHDVKN5VLINKE 172
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 183 TSEFDKFKYKVV5VLDD--VIPEILGKITLAVKALNHLKENLKTIHRDIKPSNILLDRS 240
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 173 GHYKMCDFG5SGVLVDSVAKTMDAGKCPMAAERINPELNOKGVNV5SDVMSLGITMIEM 232
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 241 GN1K1CDFG5SGVLVDSIAKTRDAGCRPMAPERIDP5AS5QGDVDRSDVMSLITILYEL 300
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 233 AILRFPE5MGTGFQDLKQVBE5PQULPAD---R5P5EPUFTQAQCLRKNA5RMSYLE 289
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 301 ATGRFPVPRKXNSVFD0LTQVWKGDPPQL5NSE5RE5P5SFINVNLCTTQD55KRPYKE 360
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 290 LMEHPFTLHKTKKTDIIA5FVKKILE 316
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 361 LUKHPFLIME5RA5V5ACVCKILDQ 387
    ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

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RESULT 14

US-09-761-569-8
; Sequence 8, Application US/09761569
; Patent No. US20020102691A1
GENERAL INFORMATION.

APPLICANT: Davis, Roger J.

; Raingeaud, Joel
 ; Gupta, Shashi
 ; Derijard, Benoit
 ;

TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE KINASES

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
C/O Fish & Richardson P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA

COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDICA ENDE PLANNING: 4:00p

```

;
; MEDIUM TYPE: Fioppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Datavision Release #1.0

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SOFTWARE: Patencin Release #1.0,
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/761,565
; FILING DATE: 16-Jan-2001

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FILED DATE: 16-JAN-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057 009

AFFILIATION NUMBER: 09/03/1,005
 FILING DATE: 1998-04-07
 ATTORNEY/AGENT INFORMATION:
 NAME: Passa, J. Peter

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; STRADENESS: No. US20020102691A1 Relevant
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8 :
US-09-761-569-8

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Query Match	52.6%;	Score 872.5;	DB 10;	Length 393;
Best Local Similarity	52.3%;	Pred. No. 4e-74;		
Matches 171; Conservative	59;	Mismatches 78;	Indels 19;	Gaps 5

```

QY 3 PNPBPERN-----LDSKRTFTTIDRMFEVEADLVTJSLDKGAAGVEKXVHA 55
      ::::: ::::: ::::: ::::: :::::
Db 57 PNPBTQONPHIERLRTTHSISSGKGLKISPEOHMFPTAEIDLDTLGEIRGAAGSVNKKVHK 116
      ::::: ::::: ::::: ::::: :::::
QY 56 OSGTMAVVRIBATVNSOEKRLMDLDIRNRYDCCFTYVFGYALPREGVWVMCMELMD 115
      ::::: ::::: ::::: ::::: :::::
Db 117 PSCQIMAVKRIISYDKEKQKOLMDLWVNRSSDCPIYVFGALPREGDCVMCMELMS 176
      ::::: ::::: ::::: ::::: :::::
QY 116 TSLDKFYR---KYLDKNNTIPEDILGEIIVASIVRALEHLHSKLSVHRDVKPSVNLINKE 172
      ::::: ::::: ::::: ::::: :::::
Db 177 TSPDFKFKYKVSVLDD--VIPETIIGKITTLTAVKALMLKLENKLTIHRIIDKPSNILLDRS 234
      ::::: ::::: ::::: ::::: :::::
QY 173 GHVKNMDEPISGVLDVSVAKTMDACKRCRYMAPERINPELNOKGVNKSVDWVSGITMIEM 233
      ::::: ::::: ::::: ::::: :::::
Db 235 GWIKLCDFEISQVLVDISAKTRDACKRCRYMAPERIDFSASQGVYVNSDWSVLSLITLYEL 294
      ::::: ::::: ::::: ::::: :::::
QY 233 ALIRPEYESWGPFFOOLKQVWEESPOLPAD--RFSPEDFVFTAOCLRKNAERMSYLE 288
      ::::: ::::: ::::: ::::: :::::
Db 295 AGRGFYPMKMSNVFQOLQVWGDPEPQLSNBSEREFSPSFINFVNLCTIKDESKRPRYKE 355
      ::::: ::::: ::::: ::::: :::::
QY 290 LMENPFPLHKTUKTDIDIAFVKYKILIGE 316
      ::::: ::::: ::::: :::::
Db 355 LKHPRFIMYEEERAVEVACVCKKILDQ 381
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RESULT 15

US-10-137-953-21
; Sequence 21, Application US/10137953
; Publication No. US20030129606A1
ORIGINAL SUBMISSION

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;
; GENERAL INFORMATION:
;
; APPLICANT: Davis, Roger J.
; Whitmarsh, Alan
;

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Tournier, Cathy
TITLE OF INVENTION: STRESS-, AND ONCOPROTEIN-
ACTIVATED HUMAN PROTEIN KINASE KINASES

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
ADDRESS: 335 Franklin Street
NEW YORK, N.Y. 10014

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA

COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDICAL TYPE: Diabetes

MEDIUM LIFE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 1.0

SOFTWARE: FASTSEEQ101 WINDOWS VER
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137, 95
FILING DATE: 03-May-2002

FILING DATE: 05-May-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/888,422
 FILING DATE: 07-JUN-1997

FILING DATE: 08/08/1995
 APPLICATION NUMBER: 08/530,950
 FILING DATE: 19-SEP-1995
 APPLICATION NUMBER: 08/446,083

FILED DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.


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?
? TELEFAX: 617/542-8906
?
? TELEX: 299354
?
? INFORMATION FOR SEQ ID NO: 21:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 393 amino acids
?
? TYPE: amino acid
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 21:
?
US-10-137-953-21

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Query Match	42.0%;	Score 697;	DB 16;	Length 393;
Best Local Similarity	45.48%;	Score 741;	DB 16;	Length 393;

[illegible]

Search completed: November 5, 2003, 20:10:56
Job time : 43 secs

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RESULT 2

S71631

mitogen-activated protein kinase kinase (EC 2.7.1.-) 6 [similarity] - human
N:Alternate names: MAP kinase kinase SAPK3
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 08-Sep-2000

C:Accession: S71631, A59347

R:Cuenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.R.
EMBO J. 15, 4156-4164, 1996

A:Title: Purification and cDNA cloning of SAPK3, the major activator of RK/p38 in stress
F:51-314/Domain: protein kinase ATP-binding motif

A:Reference number: S71631, MUID:97015116, PMID:8861944

A:Accession: S71631

A:Molecule type: mRNA

A:Residues: 1-334 <CUE>

A:Cross-references: EMBL:X96757; NID:g1495484; PIDN:CAA65532.1; PID:g1495485
A:Experimental source: cell type B cell; cell line BUB

J.Han, J.; Lee, J.D.; Jiang, Y.; Li, Z.; Feng, L.; Ulevitch, R.J.
J. Biol. Chem. 271, 2886-2891, 1996

A:Title: Characterization of the structure and function of a novel MAP kinase kinase (MK
A:Reference number: A59347, MUID:96216353, PMID:8621675

A:Accession: A59347

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
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A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
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A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
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A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Accession: GB:U39064

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>
A:Cross-references: GB:U39064; NID:g1209670; PIDN:AAB03708.1; PID:g1209671

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
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A:Experimental source: cell type fibroblast
C:Genetics:

A:Accession: S71632

A:Molecule type: mRNA

A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702
A:Experimental source: cell type fibroblast

A:Reference number: S71631, MUID:97015116, PMID:8861944
A:Accession: S71632

A:Status: nucleic acid sequence not shown

A:Residues: 1-334 <CUE>
A:Cross-references: EMBL:X97052; NID:g1495701; PIDN:CAA65764.1; PID:g1495702

A:Experimental source: cell type fibroblast
C:Genetics:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 5, 2003, 20:02:42 ; Search time 18 Seconds
(without alignments)
1698.980 Million cell updates/sec

Title: US-09-761-569-2

Perfect score: 1660

Sequence: 1 MSKPPAPNPPTPPRNLDSTRTF.....HKTCTDIAAFVKILGSDS 318

Scoring table: BLOSUM62

GAPOP 10.0 , GAPEXT 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1653	99.6	318	2	A55556
2	1359	81.9	334	2	S71631
3	1347	81.1	334	2	S71632
4	888.5	53.5	399	2	I18901
5	882	53.1	445	2	S36039
6	880	53.0	457	2	A54694
7	847	51.0	395	2	S52423
8	830.5	50.0	343	2	T16665
9	748	45.1	162	2	S71653
10	613	36.9	505	2	T16583
11	602.5	36.3	363	2	T2107
12	598	36.0	605	2	S18648
13	593	35.7	359	2	T26025
14	582.5	35.1	1218	2	T29915
15	573	34.5	393	1	A45100
16	573	34.5	393	1	JN0840
17	573	34.5	393	1	I59571
18	572	34.5	393	1	S42068
19	570.5	34.4	668	2	S56909
20	569.5	34.3	401	1	I52829
21	565	34.0	400	1	A46723
22	564	34.0	400	1	A48081
23	563	33.9	393	1	S46361
24	563	33.9	395	1	S36186
25	550	33.1	397	1	S41054
26	545.5	32.9	393	1	A45176
27	521	31.4	355	2	T02056
28	510.5	30.8	444	2	A56708
29	506	30.5	435	2	T37324

30	500	30.1	387	1	A56466	mitogen-activated
31	489	29.5	354	2	T04252	mitogen-activated
32	488.5	29.4	448	2	T16256	hypothetical prote
33	476.5	28.7	357	2	T06583	protein kinase MEK
34	467.5	28.2	363	2	T08542	mitogen-activated
35	466.5	28.1	363	2	T51735	mitogen-activated
36	466	28.1	363	2	T51992	MAP kinase kinase
37	462	27.8	363	2	T51294	MAP kinase kinase
38	452	27.2	506	2	S69045	protein kinase MKK
39	452	27.2	508	2	A48069	protein kinase MKK
40	450.5	27.1	518	2	S53804	protein kinase NPK
41	447	26.9	515	2	A25048	regulatory protein
42	433.5	26.1	340	1	OKBYR1	protein kinase byr
43	418.5	25.2	520	2	T51338	mitogen-activated
44	366.5	22.1	366	2	T51339	mitogen-activated
45	365.5	22.0	449	2	T16259	hypothetical prote

ALIGNMENTS

RESULT 1
A55556
mitogen-activated protein kinase kinase (EC 2.7.1.1) 3 [similarity] - human
N:Alternate names: MAP kinase kinase 3 (MKK3)
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Sep-2000
C:Accession: A55556
R:Derilard, B.; Raligeaud, J.; Barret, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, R.
Science 267, 682-685, 1995
A:Title: Independent human MAP kinase signal transduction pathways defined by MEK and
A:Reference number: A55556; MUID:95141073; PMID:7839144
A:Accession: A55556
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-318 <EBR>
A:Cross-references: GB:136719; NID:9685173; PIDN:AMC41718.1; PID:9685174
C:Genetics:
A:Gene: GDB:MAP2K3; PRKMK3; MEK3; MKK3
A:Cross-references: GDB:9539640; OMIM:602315
A:Map position: 17q11.2-17q11.2
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:33-296/Domain: protein kinase homology <KIN>
F:41-49/Region: protein kinase ATP-binding motif

Query Match 99.6%; Score 1653; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.4e-76;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSKPPAPNPPTPPRNLDSTRTFTTTGDRMFVEADDLVTISLGRAYGVKVRNAGSTI	60
DB	1	MSKPPAPNPPTPPRNLDSTRTFTTTGDRNFEVADDLVTISLGRAYGVKVRNAGSTI	60
QY	61	MAVRIKATVNSOQKRLMDLDINMTVOCFYVTFYGLAFREGDVMICMLDSTLDK	120
DB	61	MAVRIKATVNSOQKRLMDLDINMTVOCFYVTFYGLAFREGDVMICMLDSTLDK	120
QY	121	FYRKVLDDKMTIPEDILGEIIVSLALBHLHSKLSVIHRDVKPSNVLLINKEGHVKNCDF	180
DB	121	FYRKVLDDKMTIPEDILGEIIVSLALBHLHSKLSVIHRDVKPSNVLLINKEGHVKNCDF	180
QY	181	GISGYLVDSVAKTMDAGCKRYMAPERINPELNQKGVKSDVWSLGTITMELMRPYE	240
DB	181	GISGYLVDSVAKTMDAGCKRYMAPERINPELNQKGVKSDVWSLGTITMELMRPYE	240
QY	241	SWGTFPQQLKOVVEBPOLPADRFSPEDFTAGCCRKAPARMSTLMEHPFTLHK	300
DB	241	SWGTFPQQLKOVVEBPOLPADRFSPEDFTAGCCRKAPARMSTLMEHPFTLHK	300
QY	301	TKKTDIAAFVKILGSDS 318	
DB	301	TKKTDIAAFVKILGSDS 318	

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DB 153 RIRATVNTQOKRLMDLDSMTVDGFTVTYFGALFRGVDWICMELMDTSLDKFYKQ 212
QY 125 VLDKMTIPEDILGELIASIVRALHLSKLSVYHRDVKPSNVLINKEGHVKKMCDPFGISG 184
DB 213 VHEKGMTIPEDILGKITVSIVKALEHLSNLSVYHRDVKPSNVLINNOGVKKMCDPFGISG 272
QY 185 YLVDVSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSWGT 244
DB 273 YLVDVSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSWGT 332
QY 245 PFQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNPAERMSYLEMEHPFTLHKTKT 304
DB 333 PFQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNKSPERTYTELMQHPFTLHSDKOT 392
QY 305 DIAAFVKILGE 316
DB 393 DVASFVKSLIGD 404

RESULT 2
O9DGE0 PRELIMINARY; PRT; 363 AA.
ID O9DGE0
AC O9DGE0;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE MKK3.
GN MAP2K3 OR ZMKK3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RX SEQUENCE FROM N.A.
RP MEDLINE=20451058; PubMed=10995439;
RA Fujii R., Yamashita S., Hibi M., Hirano T.;
RT "Asymmetric p38 Activation in Zebrafish: Its Possible Role in
RT Symmetric and Synchronous Cleavage.";
CC J. Cell Biol. 150:1335-1348(2000).
CL -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: A030899; BAB1809.1; -.
DR ZFIN: ZDB-GENE-010202-3; map2k3.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 363 AA; 40807 MW; 02A7CD9A6F5A2D2C CRC64;

Query Match 83.5%; Score 1386; DB 13; Length 363;
Best Local Similarity 82.7%; Pred. No. 1,le-114;
Matches 258; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 5 PABNPPTPRNMDSRFTITIGDRMEFEVADLVITISELGRGAYGVKVRHAQSGTINAV 64
DB 52 PABNPPTPRNMDSRFTITIGDRMEFEVADLVITISELGRGAYGVKVRHAQSGTINAV 111
QY 65 RIRATVNTQOKRLMDLDSMTVDGFTVTYFGALFRGVDWICMELMDTSLDKFYKQ 124
DB 112 RIRATVNTQOKRLMDLDSMTVDGFTVTYFGALFRGVDWICMELMDTSLDKFYKQ 171
QY 125 VLDKMTIPEDILGELIASIVRALHLSKLSVYHRDVKPSNVLINKEGHVKKMCDPFGISG 184
DB 172 VHEKGMTIPEDILGKITVSIVKALEHLSNLSVYHRDVKPSNVLINNOGVKKMCDPFGISG 231
QY 185 YLVDVSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSWGT 244
DB 232 YLVDVSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSWGT 291

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QY 245 PFQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNPAERMSYLEMEHPFTLHKTKT 304
DB 292 PFQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNKSPERTYTELMQHPFTLHSDKOT 351
QY 305 DIAAFVKILGE 316
DB 352 DVASFVKSLIGD 363

RESULT 3
O9PM48 PRELIMINARY; PRT; 335 AA.
ID O9PM48
AC O9PM48;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE MAP kinase activator XMEK3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RX SEQUENCE FROM N.A.
RP MEDLINE=20065138; PubMed=10597270;
RA Kieran M.W., Katz S., Vail B., Zon L.I., Mayer B.J.;
RT "Concentration-dependent positive and negative regulation of a MAP
RT kinase by a MAP kinase kinase.";
RL Oncogene 18:6647-6657(1999).
RN [1]
RP SEQUENCE FROM N.A.
RA Kieran M., Vail B., Zon L.I., Mayer B.;
RT Submitted (Jul-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF172848; AAD4921.1; -.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 335 AA; 37923 MW; 29369A6D25B4DB57 CRC64;

Query Match 82.6%; Score 1371; DB 13; Length 335;
Best Local Similarity 81.8%; Pred. No. 2e-113;
Matches 257; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 3 KPPAPNPPTPRNMDSRFTITIGDRMEFEVADLVITISELGRGAYGVKVRHAQSGTINAV 62
DB 22 KPPAPNPPTPRNMDSRFTITIGDRMEFEVADLVITISELGRGAYGVKVRHAQSGTINAV 81
QY 63 VRIIRATVNTQOKRLMDLDSMTVDGFTVTYFGALFRGVDWICMELMDTSLDKFY 122
DB 82 VRIIRATVNTQOKRLMDLDSMTVDGFTVTYFGALFRGVDWICMELMDTSLDKFY 141
QY 123 RKLVDKMTIPEDILGELIASIVRALHLSKLSVYHRDVKPSNVLINKEGHVKKMCDPFGISG 182
DB 142 KVIDKGLTIPEDILGKITVSIVKALEHLSNLSVYHRDVKPSNVLINNOGVKKMCDPFGISG 201
QY 183 SGYLVDSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSW 242
DB 202 SGYLVDSVAKTMDACKCPYMAPERINPELNQKGYNVKSDVMSLGTITMELALRPFYDSW 261
QY 243 GTFPQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNPAERMSYLEMEHPFTLHKTK 302
DB 262 GTFPQOLKQVVEEESPQOLPADRSPPEFVDFTQAOLCKRKNKSPERTYTELMQHPFTLHSDK 321
QY 303 KTDIAFVKILGE 316

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OM protein - protein search, using sw model

Run on: November 5, 2003, 20:02:02 ; Search time 28 Seconds
(without alignments)
2930.740 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPPTPPNLDSTRTF.....HKTKKTDIAAFVKKILGSDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTREMBL_23.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phase.*
11: sp_plant.*
12: sp_proteus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacterioph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	84.0	404	13	Q91959 cyprinus ca
2	1386	83.5	363	13	Q9DGE0 brachydantio
3	1371	82.6	335	13	Q9PW48 xenopus lae
4	1346	81.1	334	11	Q925D6 rattus norv
5	1343	80.9	334	11	Q8BP44 mus musculu
6	1199	72.2	293	11	Q8C371 mus musculu
7	1162	70.0	301	11	Q8BPR2 mus musculu
8	1078	64.9	237	11	Q60521 mus musculu
9	1044	62.9	335	5	Q9U983 drosophila
10	1038	62.5	334	5	Q62602 drosophila
11	891.5	53.7	407	13	Q8UW90 cyprinus ca
12	835.5	50.3	336	5	Q85Y19 caenorhabdi
13	823	49.6	424	5	Q61444 drosophila
14	816	49.2	281	11	Q8K2U0 mus musculu
15	816	49.2	281	13	Q9DGR7 brachydantio
16	748	45.1	162	11	P70273 mus musculu

17	694	41.8	492	5	Q18411 drosophila
18	694	41.8	1178	5	Q8S221 drosophila
19	665	40.1	419	11	Q8BSP1 mus musculu
20	664	40.0	389	11	Q35720 mus musculu
21	664	40.0	391	11	Q35872 mus musculu
22	664	40.0	419	11	Q35871 mus musculu
23	664	40.0	435	11	Q9R125 mus musculu
24	664	40.0	468	11	Q54780 mus musculu
25	664	40.0	535	11	Q8CE90 mus musculu
26	661	39.8	346	11	Q9OWG6 mus musculu
27	660.5	39.8	453	11	Q9R124 mus musculu
28	660.5	39.8	469	11	Q9R126 mus musculu
29	657.5	39.6	380	11	Q9R123 mus musculu
30	656.5	39.5	426	4	Q8IY10 homo sapien
31	655	39.5	346	11	Q35406 mus musculu
32	650.5	39.2	356	5	Q9SUF5 ancylostoma
33	644	38.8	417	13	Q8QHK7 xenopus lae
34	606	36.5	347	5	Q21307 caenorhabdi
35	593	35.7	359	5	Q01706 caenorhabdi
36	583	35.1	371	5	Q23326 caenorhabdi
37	583	35.1	411	5	Q8MP83 caenorhabdi
38	573	34.5	393	11	Q913E1 mus musculu
39	571	34.4	400	11	Q913S7 mus musculu
40	570.5	34.4	401	11	Q9D7B0 mus musculu
41	563	33.9	393	6	Q9XT09 pan troglod
42	559.5	33.7	683	3	Q96W50 debaromyce
43	555	33.4	439	11	Q8K360 mus musculu
44	551.5	33.2	448	11	Q9WWS7 mus musculu
45	547.5	33.0	448	4	Q92961 homo sapien

ALIGNMENTS

RESULT 1

Q91959 PRELIMINARY; PRT; 404 AA.
ID Q91959
AC Q91959;
DT 01-OCT-2000 (TREMURel. 15, Created)
DT 01-OCT-2000 (TREMURel. 15, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE MAP kinase kinase 6 (MKK6).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto H.;
RT "p38 MAPK cascade in fish."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC EMBL; AB023480; BAA96414.1; -
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 404 AA; 45370 MW; 698435PF24057059 CRC64;

Query Match 84.0%; Score 1395; DB 13; Length 404;
Best Local Similarity 83.3%; Pred. No. 2e-115;
Matches 260; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 5 PAPPPTPPNLDSTFTTIDGRMEVEADLVITSEIGRAGYGVKEVRRASQSTIAVAK 64
DB 93 PAPPPTPPNLDSTFTTIDGRMEVEADLVITSEIGRAGYGVKEVRRASQSTIAVAK 152
QY 65 RIRATVNSQEKRLMDLDINMRTVDCFYIVTFYGFALFRGDVWICMELMDTSLDKFYRK 124

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP MUTAGENESIS OF SER-218 AND THR-222.
RX MEDLINE=96182129; PubMed=8622669;
RA Raingeaud J., Whitmarsh A.J., Barrett T., Derijard B., Davis R.J.;
RT "MKK3- and MKK6-regulated gene expression is mediated by the p38
mitogen-activated protein kinase signal transduction pathway.";
RL Mol. Cell. Biol. 16:1247-1255 (1996).
RN [6]
RP VARIANTS COLON CANCER TRP-175 AND VAL-215.
RX MEDLINE=21309069; PubMed=11414763;
RA Teng D.-H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.C.;
RT "Mutation analyses of 268 candidate genes in human tumor cell lines.";
RL Genomics 74:352-364 (2001).
CC -!- FUNCTION: Dual specificity kinase. Is activated by cytokines and
environmental stress in vivo. Catalyzes the concomitant
phosphorylation of a threonine and a tyrosine residue in the MAP
kinase p38.
CC -!- ENZYME REGULATION: Activated by dual phosphorylation on Ser-218
and Thr-222.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=3; Synonyms=3b;
CC IsoId=P46734-1; Sequences=Displayed;
CC Name=1;
CC IsoId=P46734-2; Sequence=VSP_004878;
CC Name=2; Synonyms=3c;
CC IsoId=P46734-3; Sequences=VSP_004877;
CC -!- TISSUE SPECIFICITY: Abundant expression is seen in the skeletal
muscle. It is also widely expressed in other tissues.
CC -!- PTM: Autophosphorylated.
CC -!- DISEASE: Defects in MAP2K3 may be involved in colon cancer.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP
KINASE KINASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).

FT MOD_RES 222 222 PHOSPHORYLATION.
FT VARSPLIC 1 16 MESPASSOPASPMOSK -> MGVOQTLSMRDSOTPHLLSIL
FT (in isoform 2).
FT /FTid=VSP_004877.
FT Missing (in isoform 1).
FT /FTid=VSP_004878.
FT R -> W (IN COLON CANCER).
FT /FTid=VAR_014208.
FT L -> V (IN COLON CANCER).
FT /FTid=VAR_014209.
FT S->E: CONSTITUTIVE ACTIVATION.
FT MUTAGEN 218 218 S->A: INACTIVATION.
FT MUTAGEN 218 218 T->E: CONSTITUTIVE ACTIVATION.
FT MUTAGEN 222 222 T->A: INACTIVATION.
FT MUTAGEN 222 222 E -> K (IN REF. 1 AND 3).
FT CONFLICT 341 341
SQ SEQUENCE 347 AA; 39318 MW; A80BA4FDF8F75A2 CRC64;
Query Match 99.3%; Score 1649; DB 1; Length 347;
Best Local Similarity 99.4%; Pred. No. 6e-116;
Matches 316; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSKPAPNPPTPRNLDSTFTITIGDRMFEVADDLVTISELGRGAYGVVEKVRHAQSGTI 60
Db 30 MSKPAPNPPTPRNLDSTFTITIGDRNFEVADDLVTISELGRGAYGVVEKVRHAQSGTI 89
QY 61 MAVKEIRATVNSQEQKRLMLDLDINMRTVDCFYTVTFYGFALFREGDVMICMLMDTSLDK 120
Db 90 MAVKEIRATVNSQEQKRLMLDLDINMRTVDCFYTVTFYGFALFREGDVMICMLMDTSLDK 149
QY 121 FYRKVLDDNMTIPEDILGEIAVSVIRALEHLHLSKLSVIRHDKVPSNVLINKEGHVKMCD 180
Db 150 FYRKVLDDNMTIPEDILGEIAVSVIRALEHLHLSKLSVIRHDKVPSNVLINKEGHVKMCD 209
QY 181 GISGYLVDVSAKTMDCGCKPYMAPERINPELNQKYNKSDVWSLGIWTMIENAILRFPYE 240
Db 210 GISGYLVDVSAKTMDCGCKPYMAPERINPELNQKYNKSDVWSLGIWTMIENAILRFPYE 269
QY 241 SWGTFFQQLKQVVEPSPQPADRESPEFVDPTAOLKRNPAERMSYLELMHPFFTLHK 300
Db 270 SWGTFFQQLKQVVEPSPQPADRESPEFVDPTAOLKRNPAERMSYLELMHPFFTLHK 329
QY 301 TKKTDIAAFVKKILGEDS 318
Db 330 TKKTDIAAFVKKILGEDS 347
RESULT 2
MPK3 MOUSE
ID MPK3 MOUSE STANDARD; PRT; 347 AA.
AC O09110; P97293; Q91VX1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dual specificity mitogen-activated protein kinase kinase 3
DE (EC 2.7.1.-) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERK kinase 3).
GN MAP2K3 OR PRKMK3 OR MKK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Neininger A., Gaestel M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97059154; PubMed=8900184;
RA Moriguchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,
RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;
RT "Purification and identification of a major activator for p38 from
osmotically shocked cells. Activation of mitogen-activated protein
kinase kinase 6 by osmotic shock, tumor necrosis factor-alpha, and
RT H2O2.";
RT

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OM protein - protein search, using sw model

Run on: November 5, 2003, 20:00:51 ; Search time 11 Seconds
(without alignments)
1359.499 Million cell updates/sec

Title: US-09-761-569-2
Perfect score: 1660
Sequence: 1 MSKPPAPNPPTPPRLDSRTF.....HKTCTDIAAFVKKILGEDS 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1649	99.3	347	1	MPK3 HUMAN
2	1613	97.2	347	1	MPK3 MOUSE
3	1359	81.9	334	1	MPK6 HUMAN
4	1347	81.1	334	1	MPK6 MOUSE
5	888.5	53.5	339	1	MPK4 HUMAN
6	882	53.1	446	1	MPK2_XENLA
7	881	53.1	397	1	MPK4 MOUSE
8	697	42.0	487	1	HEP DROME
9	670	40.4	419	1	MPK7 HUMAN
10	602.5	36.3	363	1	YR62_CABEL
11	598	36.0	605	1	WIS1_SCHPO
12	573	34.5	392	1	MPK1_HUMAN
13	573	34.5	392	1	MPK1_MOUSE
14	573	34.5	392	1	MPK1 RAT
15	572	34.5	392	1	MPK1 RABIT
16	570.5	34.4	668	1	PBS2_YEAST
17	569.5	34.3	401	1	MPK2_MOUSE
18	569	34.3	388	1	MPK1_SERCA
19	565	34.0	400	1	MPK2_HUMAN
20	564	34.0	400	1	MPK2 RAT
21	563	33.9	393	1	MPK1 CRIGR
22	563	33.9	394	1	MPK1_XENLA
23	563	33.9	398	1	MPK2_CHICK
24	550.5	33.2	448	1	MPK3_RAT
25	550	33.1	397	1	MPK2_CYPCA
26	545.5	32.9	393	1	DSOR DROME
27	517.5	31.2	438	1	MPK5_HUMAN
28	500	30.1	387	1	MEK2_CABEL
29	489.5	29.5	435	1	FUZ7_USTMA
30	482	27.8	363	1	SKH1_SCHPO
31	452	27.2	506	1	MKK2_YEAST
32	452	27.2	508	1	MKK1_YEAST
33	447	26.9	515	1	STE7_YEAST

RESULT 1

MPK3_HUMAN .
ID MPK3_HUMAN STANDARD; PRT; 347 AA.
AC P46734; Q99441; Q9UE71; Q9UE72;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dual specificity mitogen-activated protein kinase kinase 3
DE (EC 2.7.1.-) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERK kinase 3).
GN MAP2K3 OR PRKMK3 OR MKK3 OR MEK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95141073; PubMed=7839144;
RA Derjard B., Raingeaud J., Barrett T., Wu I.-H., Han J.,
RA Ulevitch R.J., Davis R.J.;
RT "Independent human MAP-kinase signal transduction pathways defined by
RT MEK and MKK isoforms.";
RL Science 267:682-685(1995).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=97059154; PubMed=8900184;
RA Moriguchi T., Toyoshima F., Gotch Y., Iwamatsu A., Irie K., Mori E.,
RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;
RT "Purification and identification of a major activator for p38 from
RT osmotically shocked cells: Activation of mitogen-activated protein
RT kinase kinase 6 by osmotic shock, tumor necrosis factor-alpha, and
RT H2O2.";
RL J. Biol. Chem. 271:26981-26988(1996).
[3]
RN SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RA Han J.;
RT Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Leukocyte;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

ALIGNMENTS

34	445	26.8	491	1	STK3_HUMAN	Q13188	homo sapien
35	433.5	26.1	340	1	BYR1_SCHPO	P10506	schizosacch
36	431.5	26.0	487	1	STK4_HUMAN	Q13043	homo sapien
37	370	22.3	968	1	STK4_HUMAN	Q94804	homo sapien
38	359	21.6	966	1	STK4_MOUSE	O55098	mus musculus
39	358	21.6	916	1	TNIK_MOUSE	P83510	mus musculus
40	358	21.6	1360	1	TNIK_HUMAN	Q9uke5	homo sapien
41	350	21.1	1332	1	M4K6_HUMAN	Q8n4c8	homo sapien
42	347	20.9	1308	1	M4K6_MOUSE	Q9jms2	mus musculus
43	346	20.8	471	1	SIDI_SCHPO	O14305	schizosacch
44	346	20.8	1239	1	M4K4_HUMAN	O95819	homo sapien
45	333	20.1	894	1	M4K3_HUMAN	Q8ivh8	homo sapien

Set	Items	Description
S1	227	AU='DAVIS ROGER J'
S2	16	S1 AND MKK3
S3	12	RD S2 (unique items)
S4	9	ANTIBOD?(10N)(MKK3)
S5	6	RD S4 (unique items)
S6	1304	ANTIBOD?(20N)(MITOGEN(W)ACTIVATED(W)PROTEIN(W)KINASE?)
S7	700	S6 AND (ANTIBOD?)(30N)(TREAT? OR THERAP? OR INHIBIT? OR SU- PPRESS? OR MODULAT? OR PREVENT?)
S8	47	S7 AND REVIEW?
S9	46	RD S8 (unique items)
S10	29	S7 AND (KINASE? OR MKK?)(20N)(DISEASE? OR DISORDER?)
S11	24	RD S10 (unique items)
S12	54	MKK? (20N)(DISEASE? OR DISORDER?)
S13	31	RD S12 (unique items)
S14	626	MKK3
S15	116	MKK3 AND (DISEASE? OR DISORDER?)
S16	76	RD S15 (unique items)
?		

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